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(54) Title: YIELD-RELATED POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS

(57) Abstract: The invention relates to plant transcription factor polypeptides, polynucleotides that encode them, homologs from a variety of plant species, and methods of using the polynucleotides and polypeptides to produce transgenic plants having advantageous properties compared to a reference plant. Sequence information related to these polynucleotides and polypeptides can also be used in bioinformatic search methods and is also disclosed.

YIELD-RELATED POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS

This application claims the benefit of US Provisional Application No. 60/310,847, filed August 9, 2001, US Provisional Application No. 60/336,049, filed December 5, 2001, US Provisional Application No. 60/338,692, filed December 11, 2001, and US Non-provisional Application No. 10/171,468, filed June 14, 2002, the entire contents of which are hereby incorporated by reference.

FIELD OF THE INVENTION

This invention relates to the field of plant biology. More particularly, the present invention pertains to compositions and methods for phenotypically modifying a plant.

INTRODUCTION

A plant's traits, such as its biochemical, developmental, or phenotypic characteristics, may be controlled through a number of cellular processes. One important way to manipulate that control is through transcription factors - proteins that influence the expression of a particular gene or sets of genes. Transformed and transgenic plants that comprise cells having altered levels of at least one selected transcription factor, for example, possess advantageous or desirable traits. Strategies for manipulating traits by altering a plant cell's transcription factor content can therefore result in plants and crops with commercially valuable properties. Applicants have identified polynucleotides encoding transcription factors, developed numerous transgenic plants using these polynucleotides, and have analyzed the plants for a variety of important traits. In so doing, applicants have identified important polynucleotide and polypeptide sequences for producing commercially valuable plants and crops as well as the methods for making them and using them. Other aspects and embodiments of the invention are described below and can be derived from the teachings of this disclosure as a whole.

BACKGROUND OF THE INVENTION

Transcription factors (TFs) can modulate gene expression, either increasing or decreasing (inducing or repressing) the rate of transcription. This modulation results in differential levels of gene expression at various developmental stages, in different

tissues and cell types, and in response to different exogenous (e.g., environmental) and endogenous stimuli throughout the life cycle of the organism.

Because transcription factors are key controlling elements of biological pathways, altering the expression levels of one or more transcription factors can change entire biological pathways in an organism. For example, manipulation of the levels of selected transcription factors may result in increased expression of economically useful proteins or metabolic chemicals in plants or to improve other agriculturally relevant characteristics. Conversely, blocked or reduced expression of a transcription factor may reduce biosynthesis of unwanted compounds or remove an undesirable trait. Therefore, manipulating transcription factor levels in a plant offers tremendous potential in agricultural biotechnology for modifying a plant's traits.

The present invention provides novel transcription factors useful for modifying a plant's phenotype in desirable ways.

SUMMARY OF THE INVENTION

In a first aspect, the invention relates to a recombinant polynucleotide comprising a nucleotide sequence selected from the group consisting of: (a) a nucleotide sequence encoding a polypeptide comprising a polypeptide sequence selected from those of the Sequence Listing, SEQ ID NOs:2 to 2N, where N = 2-561, or those listed in Table 4, or a complementary nucleotide sequence thereof; (b) a nucleotide sequence encoding a polypeptide comprising a variant of a polypeptide of (a) having one or more, or between 1 and about 5, or between 1 and about 10, or between 1 and about 30, conservative amino acid substitutions; (c) a nucleotide sequence comprising a sequence selected from those of SEQ ID NOs:1 to (2N - 1), where N = 2-561, or those included in Table 4, or a complementary nucleotide sequence thereof; (d) a nucleotide sequence comprising silent substitutions in a nucleotide sequence of (c); (e) a nucleotide sequence which hybridizes under stringent conditions over substantially the entire length of a nucleotide sequence of one or more of: (a), (b), (c), or (d); (f) a nucleotide sequence comprising at least 10 or 15, or at least about 20, or at least about 30 consecutive nucleotides of a sequence of any of (a)-(e), or at least 10 or 15, or at least about 20, or at least about 30 consecutive nucleotides outside of a region encoding a conserved domain of any of (a)-(e); (g) a

nucleotide sequence comprising a subsequence or fragment of any of (a)-(f), which subsequence or fragment encodes a polypeptide having a biological activity that modifies a plant's characteristic, functions as a transcription factor, or alters the level of transcription of a gene or transgene in a cell; (h) a nucleotide sequence having at least 31% sequence identity to a nucleotide sequence of any of (a)-(g); (i) a nucleotide sequence having at least 60%, or at least 70 %, or at least 80 %, or at least 90 %, or at least 95 % sequence identity to a nucleotide sequence of any of (a)-(g) or a 10 or 15 nucleotide, or at least about 20, or at least about 30 nucleotide region of a sequence of (a)-(g) that is outside of a region encoding a conserved domain; (j) a nucleotide sequence that encodes a polypeptide having at least 31% sequence identity to a polypeptide listed in Table 4, or the Sequence Listing; (k) a nucleotide sequence which encodes a polypeptide having at least 60%, or at least 70 %, or at least 80%, or at least 90 %, or at least 95 % sequence identity to a polypeptide listed in Table 4, or the Sequence Listing; and (l) a nucleotide sequence that encodes a conserved domain of a polypeptide having at least 85%, or at least 90%, or at least 95%, or at least 98% sequence identity to a conserved domain of a polypeptide listed in Table 4, or the Sequence Listing. The recombinant polynucleotide may further comprise a constitutive, inducible, or tissue-specific promoter operably linked to the nucleotide sequence. The invention also relates to compositions comprising at least two of the above-described polynucleotides.

In a second aspect, the invention comprises an isolated or recombinant polypeptide comprising a subsequence of at least about 10, or at least about 15, or at least about 20, or at least about 30 contiguous amino acids encoded by the recombinant or isolated polynucleotide described above, or comprising a subsequence of at least about 8, or at least about 12, or at least about 15, or at least about 20, or at least about 30 contiguous amino acids outside a conserved domain.

In a third aspect, the invention comprises an isolated or recombinant polynucleotide that encodes a polypeptide that is a paralog of the isolated polypeptide described above. In one aspect, the invention is an paralog which, when expressed in *Arabidopsis*, modifies a trait of the *Arabidopsis* plant.

In a fourth aspect, the invention comprises an isolated or recombinant polynucleotide that encodes a polypeptide that is an ortholog of the isolated polypeptide described above. In one aspect, the invention is an ortholog which, when expressed in *Arabidopsis*, modifies a trait of the *Arabidopsis* plant.

In a fifth aspect, the invention comprises an isolated polypeptide that is a paralog of the isolated polypeptide described above. In one aspect, the invention is an paralog which, when expressed in *Arabidopsis*, modifies a trait of the *Arabidopsis* plant.

In a sixth aspect, the invention comprises an isolated polypeptide that is an ortholog of the isolated polypeptide described above. In one aspect, the invention is an ortholog which, when expressed in *Arabidopsis*, modifies a trait of the *Arabidopsis* plant.

The present invention also encompasses transcription factor variants. A preferred transcription factor variant is one having at least 40% amino acid sequence identity, a more preferred transcription factor variant is one having at least 50% amino acid sequence identity and a most preferred transcription factor variant is one having at least 65% amino acid sequence identity to the transcription factor amino acid sequence SEQ ID NOs:2 to 2N, where N = 2-561, and which contains at least one functional or structural characteristic of the transcription factor amino acid sequence. Sequences having lesser degrees of identity but comparable biological activity are considered to be equivalents.

In another aspect, the invention is a transgenic plant comprising one or more of the above-described isolated or recombinant polynucleotides. In yet another aspect, the invention is a plant with altered expression levels of a polynucleotide described above or a plant with altered expression or activity levels of an above-described polypeptide. Further, the invention is a plant lacking a nucleotide sequence encoding a polypeptide described above or substantially lacking a polypeptide described above. The plant may be any plant, including, but not limited to, Arabidopsis, mustard, soybean, wheat, corn, potato, cotton, rice, oilseed rape, sunflower, alfalfa, sugarcane, turf, banana, blackberry, blueberry, strawberry,

raspberry, cantaloupe, carrot, cauliflower, coffee, cucumber, eggplant, grapes, honeydew, lettuce, mango, melon, onion, papaya, peas, peppers, pineapple, pumpkin, spinach, squash, sweet corn, tobacco, tomato, watermelon, rosaceous fruits, vegetable brassicas, and mint or other labiates. In yet another aspect, the inventions is an isolated plant material of a plant, including, but not limited to, plant tissue, fruit, seed, plant cell, embryo, protoplast, pollen, and the like. In yet another aspect, the invention is a transgenic plant tissue culture of regenerable cells, including, but not limited to, embryos, meristematic cells, microspores, protoplast, pollen, and the like.

In yet another aspect the invention is a transgenic plant comprising one or more of the above described polynucleotides wherein the encoded polypeptide is expressed and regulates transcription of a gene.

In a further aspect the invention provides a method of using the polynucleotide composition to breed a progeny plant from a transgenic plant including crossing plants, producing seeds from transgenic plants, and methods of breeding using transgenic plants, the method comprising transforming a plant with the polynucleotide composition to create a transgenic plant, crossing the transgenic plant with another plant, selecting seed, and growing the progeny plant from the seed.

In a further aspect, the invention provides a progeny plant derived from a parental plant wherein said progeny plant exhibits at least three fold greater messenger RNA levels than said parental plant, wherein the messenger RNA encodes a DNA-binding protein which is capable of binding to a DNA regulatory sequence and inducing expression of a plant trait gene, wherein the progeny plant is characterized by a change in the plant trait compared to said parental plant. In yet a further aspect, the progeny plant exhibits at least ten fold greater messenger RNA levels compared to said parental plant. In yet a further aspect, the progeny plant exhibits at least fifty fold greater messenger RNA levels compared to said parental plant.

In a further aspect, the invention relates to a cloning or expression vector comprising the isolated or recombinant polynucleotide described above or cells comprising the cloning or expression vector.

In yet a further aspect, the invention relates to a composition produced by incubating a polynucleotide of the invention with a nuclease, a restriction enzyme, a polymerase; a polymerase and a primer; a cloning vector, or with a cell.

Furthermore, the invention relates to a method for producing a plant having a modified trait. The method comprises altering the expression of an isolated or recombinant polynucleotide of the invention or altering the expression or activity of a polypeptide of the invention in a plant to produce a modified plant, and selecting the modified plant for a modified trait. In one aspect, the plant is a monocot plant. In another aspect, the plant is a dicot plant. In another aspect the recombinant polynucleotide is from a dicot plant and the plant is a monocot plant. In yet another aspect the recombinant polynucleotide is from a monocot plant and the plant is a dicot plant. In yet another aspect the recombinant polynucleotide is from a monocot plant and the plant is a monocot plant. In yet another aspect the recombinant polynucleotide is from a dicot plant and the plant is a dicot plant.

In another aspect, the invention is a transgenic plant comprising an isolated or recombinant polynucleotide encoding a polypeptide wherein the polypeptide is selected from the group consisting of SEQ ID NOs: 2 - 2N, where N = 2-561. In yet another aspect, the invention is a plant with altered expression levels of a polypeptide described above or a plant with altered expression or activity levels of an above-described polypeptide. Further, the invention is a plant lacking a polynucleotide sequence encoding a polypeptide described above or substantially lacking a polypeptide described above. The plant may be any plant, including, but not limited to, Arabidopsis, mustard, soybean, wheat, corn, potato, cotton, rice, oilseed rape, sunflower, alfalfa, sugarcane, turf, banana, blackberry, blueberry, strawberry, raspberry, cantaloupe, carrot, cauliflower, coffee, cucumber, eggplant, grapes, honeydew, lettuce, mango, melon, onion, papaya, peas, peppers, pineapple, pumpkin, spinach, squash, sweet corn, tobacco, tomato, watermelon, rosaceous fruits, vegetable brassicas, and mint or other labiates. In yet another aspect, the inventions is an isolated plant material of a plant, including, but not limited to, plant tissue, fruit, seed, plant cell, embryo, protoplast, pollen, and the like. In yet another aspect, the

invention is a transgenic plant tissue culture of regenerable cells, including, but not limited to, embryos, meristematic cells, microspores, protoplast, pollen, and the like.

In another aspect, the invention relates to a method of identifying a factor that is modulated by or interacts with a polypeptide encoded by a polynucleotide of the invention. The method comprises expressing a polypeptide encoded by the polynucleotide in a plant; and identifying at least one factor that is modulated by or interacts with the polypeptide. In one embodiment the method for identifying modulating or interacting factors is by detecting binding by the polypeptide to a promoter sequence, or by detecting interactions between an additional protein and the polypeptide in a yeast two hybrid system, or by detecting expression of a factor by hybridization to a microarray, subtractive hybridization, or differential display.

In yet another aspect, the invention is a method of identifying a molecule that modulates activity or expression of a polynucleotide or polypeptide of interest. The method comprises placing the molecule in contact with a plant comprising the polynucleotide or polypeptide encoded by the polynucleotide of the invention and monitoring one or more of the expression level of the polynucleotide in the plant, the expression level of the polypeptide in the plant, and modulation of an activity of the polypeptide in the plant.

In yet another aspect, the invention relates to an integrated system, computer or computer readable medium comprising one or more character strings corresponding to a polynucleotide of the invention, or to a polypeptide encoded by the polynucleotide. The integrated system, computer or computer readable medium may comprise a link between one or more sequence strings to a modified plant trait.

In yet another aspect, the invention is a method for identifying a sequence similar or homologous to one or more polynucleotides of the invention, or one or more polypeptides encoded by the polynucleotides. The method comprises providing a sequence database, and querying the sequence database with one or more target sequences corresponding to the one or more polynucleotides or to the one or more polypeptides to identify one or more sequence members of the database that display sequence similarity or homology to one or more of the one or more target sequences.

The method may further comprise of linking the one or more of the polynucleotides of the invention, or encoded polypeptides, to a modified plant phenotype.

BRIEF DESCRIPTION OF THE SEQUENCE LISTING, TABLES, AND FIGURE

The Sequence Listing provides exemplary polynucleotide and polypeptide sequences of the invention. The traits associated with the use of the sequences are included in the Examples.

Diskette1 is a read-only memory computer-readable diskette and contains a copy of the Sequence Listing in ASCII text format. The Sequence Listing is named "SEQLIST514442002041" and is 929 kilobytes in size. The copy of the Sequence Listing on the diskette is hereby incorporated by reference in its entirety.

Table 4 shows the polynucleotides and polypeptides identified by SEQ ID NO; Mendel Gene ID No.; conserved domain of the polypeptide; and if the polynucleotide was tested in a transgenic assay. The first column shows the polynucleotide SEQ ID NO; the second column shows the Mendel Gene ID No., GID; the third column shows the trait(s) resulting from the knock out or overexpression of the polynucleotide in the transgenic plant; the fourth column shows the category of the trait; the fifth column shows the transcription factor family to which the polynucleotide belongs; the sixth column ("Comment"), includes specific effects and utilities conferred by the polynucleotide of the first column; the seventh column shows the SEQ ID NO of the polypeptide encoded by the polynucleotide; and the eighth column shows the amino acid residue positions of the conserved domain in amino acid (AA) co-ordinates.

Table 5 lists a summary of orthologous and homologous sequences identified using BLAST (tblastx program). The first column shows the polynucleotide sequence identifier (SEQ ID NO), the second column shows the corresponding cDNA identifier (Gene ID), the third column shows the orthologous or homologous polynucleotide GenBank Accession Number (Test Sequence ID), the fourth column shows the

calculated probability value that the sequence identity is due to chance (Smallest Sum Probability), the fifth column shows the plant species from which the test sequence was isolated (Test Sequence Species), and the sixth column shows the orthologous or homologous test sequence GenBank annotation (Test Sequence GenBank Annotation).

Figure 1 shows a phylogenic tree of related plant families adapted from Daly et al. (2001 *Plant Physiology* 127:1328-1333).

Detailed Description of Exemplary Embodiments

In an important aspect, the present invention relates to polynucleotides and polypeptides, e.g. for modifying phenotypes of plants. Throughout this disclosure, various information sources are referred to and/or are specifically incorporated. The information sources include scientific journal articles, patent documents, textbooks, and World Wide Web browser-inactive page addresses, for example. While the reference to these information sources clearly indicates that they can be used by one of skill in the art, applicants specifically incorporate each and every one of the information sources cited herein, in their entirety, whether or not a specific mention of "incorporation by reference" is noted. The contents and teachings of each and every one of the information sources can be relied on and used to make and use embodiments of the invention.

It must be noted that as used herein and in the appended claims, the singular forms "a," "an," and "the" include plural reference unless the context clearly dictates otherwise. Thus, for example, a reference to "a plant" includes a plurality of such plants, and a reference to "a stress" is a reference to one or more stresses and equivalents thereof known to those skilled in the art, and so forth.

The polynucleotide sequences of the invention encode polypeptides that are members of well-known transcription factor families, including plant transcription factor families, as disclosed in Table 4. Generally, the transcription factors encoded by the present sequences are involved in cell differentiation and proliferation and the regulation of growth. Accordingly, one skilled in the art would recognize that by expressing the present sequences in a plant, one may change the expression of

autologous genes or induce the expression of introduced genes. By affecting the expression of similar autologous sequences in a plant that have the biological activity of the present sequences, or by introducing the present sequences into a plant, one may alter a plant's phenotype to one with improved traits. The sequences of the invention may also be used to transform a plant and introduce desirable traits not found in the wild-type cultivar or strain. Plants may then be selected for those that produce the most desirable degree of over- or underexpression of target genes of interest and coincident trait improvement.

The sequences of the present invention may be from any species, particularly plant species, in a naturally occurring form or from any source whether natural, synthetic, semi-synthetic or recombinant. The sequences of the invention may also include fragments of the present amino acid sequences. In this context, a "fragment" refers to a fragment of a polypeptide sequence which is at least 5 to about 15 amino acids in length, most preferably at least 14 amino acids, and which retain some biological activity of a transcription factor. Where "amino acid sequence" is recited to refer to an amino acid sequence of a naturally occurring protein molecule, "amino acid sequence" and like terms are not meant to limit the amino acid sequence to the complete native amino acid sequence associated with the recited protein molecule.

As one of ordinary skill in the art recognizes, transcription factors can be identified by the presence of a region or domain of structural similarity or identity to a specific consensus sequence or the presence of a specific consensus DNA-binding site or DNA-binding site motif (see, for example, Riechmann et al., (2000) *Science* 290: 2105-2110). The plant transcription factors may belong to one of the following transcription factor families: the AP2 (APETALA2) domain transcription factor family (Riechmann and Meyerowitz (1998) *Biol. Chem.* 379:633-646); the MYB transcription factor family (Martin and Paz-Ares, (1997) *Trends Genet.* 13:67-73); the MADS domain transcription factor family (Riechmann and Meyerowitz (1997) *Biol. Chem.* 378:1079-1101); the WRKY protein family (Ishiguro and Nakamura (1994) *Mol. Gen. Genet.* 244:563-571); the ankyrin-repeat protein family (Zhang et al. (1992) *Plant Cell* 4:1575-1588); the zinc finger protein (Z) family (Klug and Schwabe (1995) *FASEB J. 9:* 597-604); the homeobox (HB) protein family (Buerglin in *Guidebook to the Homeobox Genes,* Duboule (ed.) (1994) Oxford University Press);

the CAAT-element binding proteins (Forsburg and Guarente (1989) *Genes Dev.* 3:1166-1178); the squamosa promoter binding proteins (SPB) (Klein et al. (1996) *Mol. Gen. Genet.* 1996 250:7-16); the NAM protein family (Souer et al. (1996) *Cell* 85:159-170); the IAA/AUX proteins (Rouse et al. (1998) *Science* 279:1371–1373); the HLH/MYC protein family (Littlewood et al. (1994) *Prot. Profile* 1:639-709); the DNA-binding protein (DBP) family (Tucker et al. (1994) *EMBO J.* 13:2994-3002); the bZIP family of transcription factors (Foster et al. (1994) *FASEB J.* 8:192-200); the Box P-binding protein (the BPF-1) family (da Costa e Silva et al. (1993) *Plant J.* 4:125-135); the high mobility group (HMG) family (Bustin and Reeves (1996) *Prog. Nucl. Acids Res. Mol. Biol.* 54:35-100); the scarecrow (SCR) family (Di Laurenzio et al. (1996) *Cell* 86:423-433); the GF14 family (Wu et al. (1997) *Plant Physiol.* 114:1421-1431); the polycomb (PCOMB) family (Kennison (1995) *Annu. Rev. Genet.* 29:289-303); the teosinte branched (TEO) family (Luo et al. (1996) *Nature* 383:794-799; the ABI3 family (Giraudat et al. (1992) *Plant Cell* 4:1251-1261); the triple helix (TH) family (Dehesh et al. (1990) *Science* 250:1397-1399); the EIL family (Chao et al. (1997) *Cell* 89:1133-44); the AT-HOOK family (Reeves and Nissen (1990) *J. Biol. Chem.* 265:8573-8582); the S1FA family (Zhou et al. (1995) *Nucleic Acids Res.* 23:1165-1169); the bZIPT2 family (Lu and Ferl (1995) *Plant Physiol.* 109:723); the YABBY family (Bowman et al. (1999) *Development* 126:2387-96); the PAZ family (Bohmert et al. (1998) *EMBO J.* 17:170-80); a family of miscellaneous (MISC) transcription factors including the DPBF family (Kim et al. (1997) *Plant J.* 11:1237-1251) and the SPF1 family (Ishiguro and Nakamura (1994) *Mol. Gen. Genet.* 244:563-571); the golden (GLD) family (Hall et al. (1998) *Plant Cell* 10:925-936), the TUBBY family (Boggin et al, (1999) *Science* 286:2119-2125), the heat shock family (Wu C (1995) *Annu Rev Cell Dev Biol* 11:441-469), the ENBP family (Christiansen et al (1996) *Plant Mol Biol* 32:809-821), the RING-zinc family (Jensen et al. (1998) *FEBS letters* 436:283-287), the PDBP family (Janik et al *Virology.* (1989) 168:320-329), the PCF family (Cubas P, et al. *Plant J.* (1999) 18:215-22), the SRS (SHI-related) family (Fridborg et al *Plant Cell* (1999) 11:1019-1032), the CPP (cysteine-rich polycomb-like) family (Cvitanich et al *Proc. Natl. Acad. Sci.* U S A. (2000) 97:8163-8168), the ARF (auxin response factor) family (Ulmasov, et al. (1999) *Proc. Natl. Acad. Sci.* USA 96: 5844-5849), the SWI/SNF family (Collingwood et al *J. Mol. End.* 23:255-275), the ACBF family (Seguin et al (1997) *Plant Mol Biol.* 35:281-291), PCGL (CG-1 like) family (da Costa e Silva et al.

(1994) *Plant Mol Biol.* 25:921-924) the ARID family (Vazquez et al. (1999) *Development.* 126: 733-42), the Jumonji family, Balciunas et al (2000, *Trends Biochem Sci.* 25: 274-276), the bZIP-NIN family (Schauser et al (1999) *Nature* 402: 191-195), the E2F family Kaelin et al (1992) *Cell* 70: 351-364) and the GRF-like family (Knaap et al (2000) *Plant Physiol.* 122: 695-704). As indicated by any part of the list above and as known in the art, transcription factors have been sometimes categorized by class, family, and sub-family according to their structural content and consensus DNA-binding site motif, for example. Many of the classes and many of the families and sub-families are listed here. However, the inclusion of one sub-family and not another, or the inclusion of one family and not another, does not mean that the invention does not encompass polynucleotides or polypeptides of a certain family or sub-family. The list provided here is merely an example of the types of transcription factors and the knowledge available concerning the consensus sequences and consensus DNA-binding site motifs that help define them as known to those of skill in the art (each of the references noted above are specifically incorporated herein by reference). A transcription factor may include, but is not limited to, any polypeptide that can activate or repress transcription of a single gene or a number of genes. This polypeptide group includes, but is not limited to, DNA-binding proteins, DNA-binding protein binding proteins, protein kinases, protein phosphatases, GTP-binding proteins, and receptors, and the like.

In addition to methods for modifying a plant phenotype by employing one or more polynucleotides and polypeptides of the invention described herein, the polynucleotides and polypeptides of the invention have a variety of additional uses. These uses include their use in the recombinant production (i.e., expression) of proteins; as regulators of plant gene expression, as diagnostic probes for the presence of complementary or partially complementary nucleic acids (including for detection of natural coding nucleic acids); as substrates for further reactions, e.g., mutation reactions, PCR reactions, or the like; as substrates for cloning e.g., including digestion or ligation reactions; and for identifying exogenous or endogenous modulators of the transcription factors. A "polynucleotide" is a nucleic acid sequence comprising a plurality of polymerized nucleotides, e.g., at least about 15 consecutive polymerized nucleotides, optionally at least about 30 consecutive nucleotides, at least about 50 consecutive nucleotides. In many instances, a polynucleotide comprises a nucleotide

sequence encoding a polypeptide (or protein) or a domain or fragment thereof. Additionally, the polynucleotide may comprise a promoter, an intron, an enhancer region, a polyadenylation site, a translation initiation site, 5' or 3' untranslated regions, a reporter gene, a selectable marker, or the like. The polynucleotide can be single stranded or double stranded DNA or RNA. The polynucleotide optionally comprises modified bases or a modified backbone. The polynucleotide can be, e.g., genomic DNA or RNA, a transcript (such as an mRNA), a cDNA, a PCR product, a cloned DNA, a synthetic DNA or RNA, or the like. The polynucleotide can comprise a sequence in either sense or antisense orientations.

A "recombinant polynucleotide" is a polynucleotide that is not in its native state, e.g., the polynucleotide comprises a nucleotide sequence not found in nature, or the polynucleotide is in a context other than that in which it is naturally found, e.g., separated from nucleotide sequences with which it typically is in proximity in nature, or adjacent (or contiguous with) nucleotide sequences with which it typically is not in proximity. For example, the sequence at issue can be cloned into a vector, or otherwise recombined with one or more additional nucleic acid.

An "isolated polynucleotide" is a polynucleotide whether naturally occurring or recombinant, that is present outside the cell in which it is typically found in nature, whether purified or not. Optionally, an isolated polynucleotide is subject to one or more enrichment or purification procedures, e.g., cell lysis, extraction, centrifugation, precipitation, or the like.

A "polypeptide" is an amino acid sequence comprising a plurality of consecutive polymerized amino acid residues e.g., at least about 15 consecutive polymerized amino acid residues, optionally at least about 30 consecutive polymerized amino acid residues, at least about 50 consecutive polymerized amino acid residues. In many instances, a polypeptide comprises a polymerized amino acid residue sequence that is a transcription factor or a domain or portion or fragment thereof. Additionally, the polypeptide may comprise a localization domain, 2) an activation domain, 3) a repression domain, 4) an oligomerization domain or 5) a DNA-binding domain, or the like. The polypeptide optionally comprises modified

amino acid residues, naturally occurring amino acid residues not encoded by a codon, non-naturally occurring amino acid residues.

A "recombinant polypeptide" is a polypeptide produced by translation of a recombinant polynucleotide. A "synthetic polypeptide" is a polypeptide created by consecutive polymerization of isolated amino acid residues using methods well known in the art. An "isolated polypeptide," whether a naturally occurring or a recombinant polypeptide, is more enriched in (or out of) a cell than the polypeptide in its natural state in a wild type cell, e.g., more than about 5% enriched, more than about 10% enriched, or more than about 20%, or more than about 50%, or more, enriched, i.e., alternatively denoted: 105%, 110%, 120%, 150% or more, enriched relative to wild type standardized at 100%. Such an enrichment is not the result of a natural response of a wild type plant. Alternatively, or additionally, the isolated polypeptide is separated from other cellular components with which it is typically associated, e.g., by any of the various protein purification methods herein.

"Identity" or "similarity" refers to sequence similarity between two polynucleotide sequences or between two polypeptide sequences, with identity being a more strict comparison. The phrases "percent identity" and "% identity" refer to the percentage of sequence similarity found in a comparison of two or more polynucleotide sequences or two or more polypeptide sequences. Identity or similarity can be determined by comparing a position in each sequence that may be aligned for purposes of comparison. When a position in the compared sequence is occupied by the same nucleotide base or amino acid, then the molecules are identical at that position. A degree of similarity or identity between polynucleotide sequences is a function of the number of identical or matching nucleotides at positions shared by the polynucleotide sequences. A degree of identity of polypeptide sequences is a function of the number of identical amino acids at positions shared by the polypeptide sequences. A degree of homology or similarity of polypeptide sequences is a function of the number of amino acids, i.e., structurally related, at positions shared by the polypeptide sequences.

"Altered" nucleic acid sequences encoding polypeptide include those sequences with deletions, insertions, or substitutions of different nucleotides, resulting

in a polynucleotide encoding a polypeptide with at least one functional characteristic of the polypeptide. Included within this definition are polymorphisms that may or may not be readily detectable using a particular oligonucleotide probe of the polynucleotide encoding polypeptide, and improper or unexpected hybridization to allelic variants, with a locus other than the normal chromosomal locus for the polynucleotide sequence encoding polypeptide. The encoded polypeptide protein may also be "altered", and may contain deletions, insertions, or substitutions of amino acid residues that produce a silent change and result in a functionally equivalent polypeptide. Deliberate amino acid substitutions may be made on the basis of similarity in residue side chain chemistry, including, but not limited to, polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues, as long as the biological activity of polypeptide is retained. For example, negatively charged amino acids may include aspartic acid and glutamic acid, positively charged amino acids may include lysine and arginine, and amino acids with uncharged polar head groups having similar hydrophilicity values may include leucine, isoleucine, and valine; glycine and alanine; asparagine and glutamine; serine and threonine; and phenylalanine and tyrosine. Alignments between different polypeptide sequences may be used to calculate "percentage sequence similarity".

The term "plant" includes whole plants, shoot vegetative organs/structures (*e.g.*, leaves, stems and tubers), roots, flowers and floral organs/structures (*e.g.*, bracts, sepals, petals, stamens, carpels, anthers and ovules), seed (including embryo, endosperm, and seed coat) and fruit (the mature ovary), plant tissue (*e.g.*, vascular tissue, ground tissue, and the like) and cells (*e.g.*, guard cells, egg cells, and the like), and progeny of same. The class of plants that can be used in the method of the invention is generally as broad as the class of higher and lower plants amenable to transformation techniques, including angiosperms (monocotyledonous and dicotyledonous plants), gymnosperms, ferns, horsetails, psilophytes, lycophytes, bryophytes, and multicellular algae. (See for example, Figure 1, adapted from Daly et al. 2001 *Plant Physiology* 127:1328-1333; and see also Tudge, C., The Variety of Life, Oxford University Press, New York, 2000, pp. 547-606.)

A "transgenic plant" refers to a plant that contains genetic material not found in a wild type plant of the same species, variety or cultivar. The genetic material may

include a transgene, an insertional mutagenesis event (such as by transposon or T-DNA insertional mutagenesis), an activation tagging sequence, a mutated sequence, a homologous recombination event or a sequence modified by chimeraplasty. Typically, the foreign genetic material has been introduced into the plant by human manipulation, but any method can be used as one of skill in the art recognizes.

A transgenic plant may contain an expression vector or cassette. The expression cassette typically comprises a polypeptide-encoding sequence operably linked (i.e., under regulatory control of) to appropriate inducible or constitutive regulatory sequences that allow for the expression of polypeptide. The expression cassette can be introduced into a plant by transformation or by breeding after transformation of a parent plant. A plant refers to a whole plant as well as to a plant part, such as seed, fruit, leaf, or root, plant tissue, plant cells or any other plant material, e.g., a plant explant, as well as to progeny thereof, and to *in vitro* systems that mimic biochemical or cellular components or processes in a cell.

"Ectopic expression or altered expression" in reference to a polynucleotide indicates that the pattern of expression in, e.g., a transgenic plant or plant tissue, is different from the expression pattern in a wild type plant or a reference plant of the same species. The pattern of expression may also be compared with a reference expression pattern in a wild type plant of the same species. For example, the polynucleotide or polypeptide is expressed in a cell or tissue type other than a cell or tissue type in which the sequence is expressed in the wild type plant, or by expression at a time other than at the time the sequence is expressed in the wild type plant, or by a response to different inducible agents, such as hormones or environmental signals, or at different expression levels (either higher or lower) compared with those found in a wild type plant. The term also refers to altered expression patterns that are produced by lowering the levels of expression to below the detection level or completely abolishing expression. The resulting expression pattern can be transient or stable, constitutive or inducible. In reference to a polypeptide, the term "ectopic expression or altered expression" further may relate to altered activity levels resulting from the interactions of the polypeptides with exogenous or endogenous modulators or from interactions with factors or as a result of the chemical modification of the polypeptides.

A "fragment" or "domain," with respect to a polypeptide, refers to a subsequence of the polypeptide. In some cases, the fragment or domain, is a subsequence of the polypeptide which performs at least one biological function of the intact polypeptide in substantially the same manner, or to a similar extent, as does the intact polypeptide. For example, a polypeptide fragment can comprise a recognizable structural motif or functional domain such as a DNA-binding site or domain that binds to a DNA promoter region, an activation domain, or a domain for protein-protein interactions. Fragments can vary in size from as few as 6 amino acids to the full length of the intact polypeptide, but are preferably at least about 30 amino acids in length and more preferably at least about 60 amino acids in length. In reference to a polynucleotide sequence, "a fragment" refers to any subsequence of a polynucleotide, typically, of at least about 15 consecutive nucleotides, preferably at least about 30 nucleotides, more preferably at least about 50 nucleotides, of any of the sequences provided herein.

The invention also encompasses production of DNA sequences that encode transcription factors and transcription factor derivatives, or fragments thereof, entirely by synthetic chemistry. After production, the synthetic sequence may be inserted into any of the many available expression vectors and cell systems using reagents well known in the art. Moreover, synthetic chemistry may be used to introduce mutations into a sequence encoding transcription factors or any fragment thereof.

A "conserved domain", with respect to a polypeptide, refers to a domain within a transcription factor family which exhibits a higher degree of sequence homology, such as at least 65% sequence identity including conservative substitutions, and preferably at least 80% sequence identity, and more preferably at least 85%, or at least about 86%, or at least about 87%, or at least about 88%, or at least about 90%, or at least about 95%, or at least about 98% amino acid residue sequence identity of a polypeptide of consecutive amino acid residues. A fragment or domain can be referred to as outside a consensus sequence or outside a consensus DNA-binding site that is known to exist or that exists for a particular transcription factor class, family, or sub-family. In this case, the fragment or domain will not include the exact amino acids of a consensus sequence or consensus DNA-binding

site of a transcription factor class, family or sub-family, or the exact amino acids of a particular transcription factor consensus sequence or consensus DNA-binding site. Furthermore, a particular fragment, region, or domain of a polypeptide, or a polynucleotide encoding a polypeptide, can be "outside a conserved domain" if all the amino acids of the fragment, region, or domain fall outside of a defined conserved domain(s) for a polypeptide or protein. The conserved domains for each of polypeptides of SEQ ID NOs:2 - 2N, where N = 2-561, are listed in Table 4 as described in Example VII. Also, many of the polypeptides of Table 4 have conserved domains specifically indicated by start and stop sites. A comparison of the regions of the polypeptides in SEQ ID NOs:2 - 2N, where N = 2-561, or of those in Table 4, allows one of skill in the art to identify conserved domain(s) for any of the polypeptides listed or referred to in this disclosure, including those in Table 4.

A "trait" refers to a physiological, morphological, biochemical, or physical characteristic of a plant or particular plant material or cell. In some instances, this characteristic is visible to the human eye, such as seed or plant size, or can be measured by biochemical techniques, such as detecting the protein, starch, or oil content of seed or leaves, or by observation of a metabolic or physiological process, e.g. by measuring uptake of carbon dioxide, or by the observation of the expression level of a gene or genes, e.g., by employing Northern analysis, RT-PCR, microarray gene expression assays, or reporter gene expression systems, or by agricultural observations such as stress tolerance, yield, or pathogen tolerance. Any technique can be used to measure the amount of, comparative level of, or difference in any selected chemical compound or macromolecule in the transgenic plants, however.

"Trait modification" refers to a detectable difference in a characteristic in a plant ectopically expressing a polynucleotide or polypeptide of the present invention relative to a plant not doing so, such as a wild type plant. In some cases, the trait modification can be evaluated quantitatively. For example, the trait modification can entail at least about a 2% increase or decrease in an observed trait (difference), at least a 5% difference, at least about a 10% difference, at least about a 20% difference, at least about a 30%, at least about a 50%, at least about a 70%, or at least about a 100%, or an even greater difference compared with a wild type plant. It is known that there can be a natural variation in the modified trait. Therefore, the trait modification

observed entails a change of the normal distribution of the trait in the plants compared with the distribution observed in wild type plant.

I. Traits Which May Be Modified

Trait modifications of particular interest include those to seed (such as embryo or endosperm), fruit, root, flower, leaf, stem, shoot, seedling or the like, including: enhanced tolerance to environmental conditions including freezing, chilling, heat, drought, water saturation, radiation and ozone; improved tolerance to microbial, fungal or viral diseases; improved tolerance to pest infestations, including nematodes, mollicutes, parasitic higher plants or the like; decreased herbicide sensitivity; improved tolerance of heavy metals or enhanced ability to take up heavy metals; improved growth under poor photoconditions (e.g., low light and/or short day length), or changes in expression levels of genes of interest. Other phenotype that can be modified relate to the production of plant metabolites, such as variations in the production of taxol, tocopherol, tocotrienol, sterols, phytosterols, vitamins, wax monomers, anti-oxidants, amino acids, lignins, cellulose, tannins, prenyllipids (such as chlorophylls and carotenoids), glucosinolates, and terpenoids, enhanced or compositionally altered protein or oil production (especially in seeds), or modified sugar (insoluble or soluble) and/or starch composition. Physical plant characteristics that can be modified include cell development (such as the number of trichomes), fruit and seed size and number, yields of plant parts such as stems, leaves, inflorescences, and roots, the stability of the seeds during storage, characteristics of the seed pod (e.g., susceptibility to shattering), root hair length and quantity, internode distances, or the quality of seed coat. Plant growth characteristics that can be modified include growth rate, germination rate of seeds, vigor of plants and seedlings, leaf and flower senescence, male sterility, apomixis, flowering time, flower abscission, rate of nitrogen uptake, osmotic sensitivity to soluble sugar concentrations, biomass or transpiration characteristics, as well as plant architecture characteristics such as apical dominance, branching patterns, number of organs, organ identity, organ shape or size.

II. Transcription Factors Modify Expression Of Endogenous Genes

Expression of genes which encode transcription factors that modify expression of endogenous genes, polynucleotides, and proteins are well known in the art. In addition, transgenic plants comprising isolated polynucleotides encoding transcription

factors may also modify expression of endogenous genes, polynucleotides, and proteins. Examples include Peng et al. (1997, Genes and Development 11:3194-3205) and Peng et al. (1999, Nature, 400:256-261). In addition, many others have demonstrated that an *Arabidopsis* transcription factor expressed in an exogenous plant species elicits the same or very similar phenotypic response. See, for example, Fu et al. (2001, Plant Cell 13:1791-1802); Nandi et al. (2000, Curr. Biol. 10:215-218); Coupland (1995, Nature 377:482-483); and Weigel and Nilsson (1995, Nature 377:482-500).

In another example, Mandel et al. (1992, Cell 71-133-143) and Suzuki et al. (2001, Plant J. 28:409-418) teach that a transcription factor expressed in another plant species elicits the same or very similar phenotypic response of the endogenous sequence, as often predicted in earlier studies of *Arabidopsis* transcription factors in *Arabidopsis* (see Mandel et al., 1992, *supra*; Suzuki et al., 2001, *supra*).

Other examples include Müller et al. (2001, Plant J. 28:169-179); Kim et al. (2001, Plant J. 25:247-259); Kyozuka and Shimamoto (2002, Plant Cell Physiol. 43:130-135); Boss and Thomas (2002, Nature, 416:847-850); He et al. (2000, Transgenic Res., 9:223-227); and Robson et al. (2001, Plant J. 28:619-631).

In yet another example, Gilmour et al. (1998, Plant J. 16:433-442) teach an Arabidopsis AP2 transcription factor, CBF1, which, when overexpressed in transgenic plants, increases plant freezing tolerance. Jaglo et al (2001, Plant Physiol. 127:910-917) further identified sequences in Brassica napus which encode CBF-like genes and that transcripts for these genes accumulated rapidly in response to low temperature. Transcripts encoding CBF-like proteins were also found to accumulate rapidly in response to low temperature in wheat, as well as in tomato. An alignment of the CBF proteins from Arabidopsis, B. napus, wheat, rye, and tomato revealed the presence of conserved amino acid sequences, PKK/RPAGRxKFxETRHP and DSAWR, that bracket the AP2/EREBP DNA binding domains of the proteins and distinguish them from other members of the AP2/EREBP protein family. (See Jaglo et al., supra.)

III. Polypeptides and Polynucleotides of the Invention

The present invention provides, among other things, transcription factors (TFs), and transcription factor homologue polypeptides, and isolated or recombinant polynucleotides encoding the polypeptides, or novel variant polypeptides or polynucleotides encoding novel variants of transcription factors derived from the specific sequences provided here. These polypeptides and polynucleotides may be employed to modify a plant's characteristic.

Exemplary polynucleotides encoding the polypeptides of the invention were identified in the *Arabidopsis thaliana* GenBank database using publicly available sequence analysis programs and parameters. Sequences initially identified were then further characterized to identify sequences comprising specified sequence strings corresponding to sequence motifs present in families of known transcription factors. In addition, further exemplary polynucleotides encoding the polypeptides of the invention were identified in the plant GenBank database using publicly available sequence analysis programs and parameters. Sequences initially identified were then further characterized to identify sequences comprising specified sequence strings corresponding to sequence motifs present in families of known transcription factors. Polynucleotide sequences meeting such criteria were confirmed as transcription factors.

Additional polynucleotides of the invention were identified by screening *Arabidopsis thaliana* and/or other plant cDNA libraries with probes corresponding to known transcription factors under low stringency hybridization conditions. Additional sequences, including full length coding sequences were subsequently recovered by the rapid amplification of cDNA ends (RACE) procedure, using a commercially available kit according to the manufacturer's instructions. Where necessary, multiple rounds of RACE are performed to isolate 5′ and 3′ ends. The full length cDNA was then recovered by a routine end-to-end polymerase chain reaction (PCR) using primers specific to the isolated 5′ and 3′ ends. Exemplary sequences are provided in the Sequence Listing.

The polynucleotides of the invention can be or were ectopically expressed in overexpressor or knockout plants and the changes in the characteristic(s) or trait(s) of

the plants observed. Therefore, the polynucleotides and polypeptides can be employed to improve the characteristics of plants.

The polynucleotides of the invention can be or were ectopically expressed in overexpressor plant cells and the changes in the expression levels of a number of genes, polynucleotides, and/or proteins of the plant cells observed. Therefore, the polynucleotides and polypeptides can be employed to change expression levels of a genes, polynucleotides, and/or proteins of plants.

IV. Producing Polypeptides

The polynucleotides of the invention include sequences that encode transcription factors and transcription factor homologue polypeptides and sequences complementary thereto, as well as unique fragments of coding sequence, or sequence complementary thereto. Such polynucleotides can be, e.g., DNA or RNA, e.g., mRNA, cRNA, synthetic RNA, genomic DNA, cDNA synthetic DNA, oligonucleotides, etc. The polynucleotides are either double-stranded or single-stranded, and include either, or both sense (i.e., coding) sequences and antisense (i.e., non-coding, complementary) sequences. The polynucleotides include the coding sequence of a transcription factor, or transcription factor homologue polypeptide, in isolation, in combination with additional coding sequences (e.g., a purification tag, a localization signal, as a fusion-protein, as a pre-protein, or the like), in combination with non-coding sequences (e.g., introns or inteins, regulatory elements such as promoters, enhancers, terminators, and the like), and/or in a vector or host environment in which the polynucleotide encoding a transcription factor or transcription factor homologue polypeptide is an endogenous or exogenous gene.

A variety of methods exist for producing the polynucleotides of the invention. Procedures for identifying and isolating DNA clones are well known to those of skill in the art, and are described in, e.g., Berger and Kimmel, Guide to Molecular Cloning Techniques, Methods in Enzymology volume 152 Academic Press, Inc., San Diego, CA ("Berger"); Sambrook et al., Molecular Cloning - A Laboratory Manual (2nd Ed.), Vol. 1-3, Cold Spring Harbor Laboratory, Cold Spring Harbor, New York, 1989 ("Sambrook") and Current Protocols in Molecular Biology, F. M. Ausubel et al., eds.,

Current Protocols, a joint venture between Greene Publishing Associates, Inc. and John Wiley & Sons, Inc., (supplemented through 2000) ("Ausubel").

Alternatively, polynucleotides of the invention, can be produced by a variety of in vitro amplification methods adapted to the present invention by appropriate selection of specific or degenerate primers. Examples of protocols sufficient to direct persons of skill through in vitro amplification methods, including the polymerase chain reaction (PCR) the ligase chain reaction (LCR), Qbeta-replicase amplification and other RNA polymerase mediated techniques (e.g., NASBA), e.g., for the production of the homologous nucleic acids of the invention are found in Berger (supra), Sambrook (supra), and Ausubel (supra), as well as Mullis et al., (1987) PCR Protocols A Guide to Methods and Applications (Innis et al. eds) Academic Press Inc. San Diego, CA (1990) (Innis). Improved methods for cloning in vitro amplified nucleic acids are described in Wallace et al., U.S. Pat. No. 5,426,039. Improved methods for amplifying large nucleic acids by PCR are summarized in Cheng et al. (1994) Nature 369: 684-685 and the references cited therein, in which PCR amplicons of up to 40kb are generated. One of skill will appreciate that essentially any RNA can be converted into a double stranded DNA suitable for restriction digestion, PCR expansion and sequencing using reverse transcriptase and a polymerase. *See*, e.g., Ausubel, Sambrook and Berger, *all supra*.

Alternatively, polynucleotides and oligonucleotides of the invention can be assembled from fragments produced by solid-phase synthesis methods. Typically, fragments of up to approximately 100 bases are individually synthesized and then enzymatically or chemically ligated to produce a desired sequence, e.g., a polynucleotide encoding all or part of a transcription factor. For example, chemical synthesis using the phosphoramidite method is described, e.g., by Beaucage et al. (1981) Tetrahedron Letters 22:1859-1869; and Matthes et al. (1984) EMBO J. 3:801-805. According to such methods, oligonucleotides are synthesized, purified, annealed to their complementary strand, ligated and then optionally cloned into suitable vectors. And if so desired, the polynucleotides and polypeptides of the invention can be custom ordered from any of a number of commercial suppliers.

V. Homologous Sequences

Sequences homologous, i.e., that share significant sequence identity or similarity, to those provided in the Sequence Listing, derived from *Arabidopsis thaliana* or from other plants of choice are also an aspect of the invention. Homologous sequences can be derived from any plant including monocots and dicots and in particular agriculturally important plant species, including but not limited to, crops such as soybean, wheat, corn, potato, cotton, rice, rape, oilseed rape (including canola), sunflower, alfalfa, sugarcane and turf; or fruits and vegetables, such as banana, blackberry, blueberry, strawberry, and raspberry, cantaloupe, carrot, cauliflower, coffee, cucumber, eggplant, grapes, honeydew, lettuce, mango, melon, onion, papaya, peas, peppers, pineapple, pumpkin, spinach, squash, sweet corn, tobacco, tomato, watermelon, rosaceous fruits (such as apple, peach, pear, cherry and plum) and vegetable brassicas (such as broccoli, cabbage, cauliflower, Brussels sprouts, and kohlrabi). Other crops, fruits and vegetables whose phenotype can be changed include barley, rye, millet, sorghum, currant, avocado, citrus fruits such as oranges, lemons, grapefruit and tangerines, artichoke, cherries, nuts such as the walnut and peanut, endive, leek, roots, such as arrowroot, beet, cassava, turnip, radish, yam, and sweet potato, and beans. The homologous sequences may also be derived from woody species, such pine, poplar and eucalyptus, or mint or other labiates.

Orthologs And Paralogs

Several different methods are known by those of skill in the art for identifying and defining these functionally homologous sequences. Three general methods for defining paralogs and orthologs are described; a paralog or ortholog or homolog may be identified by one or more of the methods described below.

Orthologs and paralogs are evolutionarily related genes that have similar sequence and similar functions. Orthologs are structurally related genes in different species that are derived from a speciation event. Paralogs are structurally related genes within a single species that are derived by a duplication event.

Within a single plant species, gene duplication may cause two copies of a particular gene, giving rise to two or more genes with similar sequence and similar function known as paralogs. A paralog is therefore a similar gene with a similar function within the same species. Paralogs typically cluster together or in the same

clade (a group of similar genes) when a gene family phylogeny is analyzed using programs such as CLUSTAL (Thompson et al. (1994) Nucleic Acids Res. 22:4673-4680; Higgins et al. (1996) Methods Enzymol. 266 383-402). Groups of similar genes can also be identified with pair-wise BLAST analysis (Feng and Doolittle (1987) J. Mol. Evol. 25:351-360). For example, a clade of very similar MADS domain transcription factors from Arabidopsis all share a common function in flowering time (Ratcliffe et al. (2001) Plant Physiol. 126:122-132), and a group of very similar AP2 domain transcription factors from Arabidopsis are involved in tolerance of plants to freezing (Gilmour et al. (1998) Plant J. 16:433-442). Analysis of groups of similar genes with similar function that fall within one clade can yield sub-sequences that are particular to the clade. These sub-sequences, known as consensus sequences, can not only be used to define the sequences within each clade, but define the functions of these genes; genes within a clade may contain paralogous or orthologous sequences that share the same function. (See also, for example, Mount, D.W. (2001) Bioinformatics: Sequence and Genome Analysis Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York page 543.)

Speciation, the production of new species from a parental species, can also give rise to two or more genes with similar sequence and similar function. These genes, termed orthologs, often have an identical function within their host plants and are often interchangeable between species without losing function. Because plants have common ancestors, many genes in any plant species will have a corresponding orthologous gene in another plant species. Once a phylogenic tree for a gene family of one species has been constructed using a program such as CLUSTAL (Thompson et al. (1994) Nucleic Acids Res. 22:4673-4680; Higgins et al. (1996) Methods Enzymol. 266:383-402), potential orthologous sequences can placed into the phylogenetic tree and its relationship to genes from the species of interest can be determined. Once the ortholog pair has been identified, the function of the test ortholog can be determined by determining the function of the reference ortholog.

Transcription factors that are homologous to the listed sequences will typically share at least about 30% amino acid sequence identity, or at least about 30% amino acid sequence identity outside of a known consensus sequence or consensus DNA-binding site. More closely related transcription factors can share at least about 50%,

about 60%, about 65%, about 70%, about 75% or about 80% or about 90% or about 95% or about 98% or more sequence identity with the listed sequences, or with the listed sequences but excluding or outside a known consensus sequence or consensus DNA-binding site, or with the listed sequences excluding one or all conserved domain. Factors that are most closely related to the listed sequences share, e.g., at least about 85%, about 90% or about 95% or more % sequence identity to the listed sequences, or to the listed sequences but excluding or outside a known consensus sequence or consensus DNA-binding site or outside one or all conserved domain. At the nucleotide level, the sequences will typically share at least about 40% nucleotide sequence identity, preferably at least about 50%, about 60%, about 70% or about 80% sequence identity, and more preferably about 85%, about 90%, about 95% or about 97% or more sequence identity to one or more of the listed sequences, or to a listed sequence but excluding or outside a known consensus sequence or consensus DNA-binding site, or outside one or all conserved domain. The degeneracy of the genetic code enables major variations in the nucleotide sequence of a polynucleotide while maintaining the amino acid sequence of the encoded protein. Conserved domains within a transcription factor family may exhibit a higher degree of sequence homology, such as at least 65% sequence identity including conservative substitutions, and preferably at least 80% sequence identity, and more preferably at least 85%, or at least about 86%, or at least about 87%, or at least about 88%, or at least about 90%, or at least about 95%, or at least about 98% sequence identity. Transcription factors that are homologous to the listed sequences should share at least 30%, or at least about 60%, or at least about 75%, or at least about 80%, or at least about 90%, or at least about 95% amino acid sequence identity over the entire length of the polypeptide or the homolog. In addition, transcription factors that are homologous to the listed sequences should share at least 30%, or at least about 60%, or at least about 75%, or at least about 80%, or at least about 90%, or at least about 95% amino acid sequence similarity over the entire length of the polypeptide or the homolog.

Percent identity can be determined electronically, e.g., by using the MEGALIGN program (DNASTAR, Inc. Madison, Wis.). The MEGALIGN program can create alignments between two or more sequences according to different methods, e.g., the clustal method. (See, e.g., Higgins, D. G. and P. M. Sharp (1988) Gene

73:237-244.) The clustal algorithm groups sequences into clusters by examining the distances between all pairs. The clusters are aligned pairwise and then in groups. Other alignment algorithms or programs may be used, including FASTA, BLAST, or ENTREZ, FASTA and BLAST. These are available as a part of the GCG sequence analysis package (University of Wisconsin, Madison, Wis.), and can be used with or without default settings. ENTREZ is available through the National Center for Biotechnology Information. In one embodiment, the percent identity of two sequences can be determined by the GCG program with a gap weight of 1, e.g., each amino acid gap is weighted as if it were a single amino acid or nucleotide mismatch between the two sequences (see USPN 6,262,333).

Other techniques for alignment are described in Methods in Enzymology, vol. 266: Computer Methods for Macromolecular Sequence Analysis (1996), ed. Doolittle, Academic Press, Inc., San Diego, Calif., USA. Preferably, an alignment program that permits gaps in the sequence is utilized to align the sequences. The Smith-Waterman is one type of algorithm that permits gaps in sequence alignments. See Methods Mol. Biol. 70: 173-187 (1997). Also, the GAP program using the Needleman and Wunsch alignment method can be utilized to align sequences. An alternative search strategy uses MPSRCH software, which runs on a MASPAR computer. MPSRCH uses a Smith-Waterman algorithm to score sequences on a massively parallel computer. This approach improves ability to pick up distantly related matches, and is especially tolerant of small gaps and nucleotide sequence errors. Nucleic acid-encoded amino acid sequences can be used to search both protein and DNA databases.

The percentage similarity between two polypeptide sequences, e.g., sequence A and sequence B, is calculated by dividing the length of sequence A, minus the number of gap residues in sequence A, minus the number of gap residues in sequence B, into the sum of the residue matches between sequence A and sequence B, times one hundred. Gaps of low or of no similarity between the two amino acid sequences are not included in determining percentage similarity. Percent identity between polynucleotide sequences can also be counted or calculated by other methods known in the art, e.g., the Jotun Hein method. (See, e.g., Hein, J. (1990) Methods Enzymol. 183:626-645.) Identity between sequences can also be determined by other methods

known in the art, e.g., by varying hybridization conditions (see US Patent Application No. 20010010913).

Thus, the invention provides methods for identifying a sequence similar or paralogous or orthologous or homologous to one or more polynucleotides as noted herein, or one or more target polypeptides encoded by the polynucleotides, or otherwise noted herein and may include linking or associating a given plant phenotype or gene function with a sequence. In the methods, a sequence database is provided (locally or across an inter or intra net) and a query is made against the sequence database using the relevant sequences herein and associated plant phenotypes or gene functions.

In addition, one or more polynucleotide sequences or one or more polypeptides encoded by the polynucleotide sequences may be used to search against a BLOCKS (Bairoch et al. (1997) Nucleic Acids Res. 25:217-221), PFAM, and other databases which contain previously identified and annotated motifs, sequences and gene functions. Methods that search for primary sequence patterns with secondary structure gap penalties (Smith et al. (1992) Protein Engineering 5:35-51) as well as algorithms such as Basic Local Alignment Search Tool (BLAST; Altschul, S. F. (1993) J. Mol. Evol. 36:290-300; Altschul et al. (1990) *supra*), BLOCKS (Henikoff, S. and Henikoff, G. J. (1991) Nucleic Acids Research 19:6565-6572), Hidden Markov Models (HMM; Eddy, S. R. (1996) Cur. Opin. Str. Biol. 6:361-365; Sonnhammer et al. (1997) Proteins 28:405-420), and the like, can be used to manipulate and analyze polynucleotide and polypeptide sequences encoded by polynucleotides. These databases, algorithms and other methods are well known in the art and are described in Ausubel et al. (1997; Short Protocols in Molecular Biology, John Wiley & Sons, New York N.Y., unit 7.7) and in Meyers, R. A. (1995; Molecular Biology and Biotechnology, Wiley VCH, New York N.Y., p 856-853).

Furthermore, methods using manual alignment of sequences similar or homologous to one or more polynucleotide sequences or one or more polypeptides encoded by the polynucleotide sequences may be used to identify regions of similarity and conserved domains. Such manual methods are well-known of those of skill in the art and can include, for example, comparisons of tertiary structure between a

polypeptide sequence encoded by a polynucleotide which comprises a known function with a polypeptide sequence encoded by a polynucleotide sequence which has a function not yet determined. Such examples of tertiary structure may comprise predicted alpha helices, beta-sheets, amphipathic helices, leucine zipper motifs, zinc finger motifs, proline-rich regions, cysteine repeat motifs, and the like.

VI. Identifying Polynucleotides or Nucleic Acids by Hybridization

Polynucleotides homologous to the sequences illustrated in the Sequence Listing and tables can be identified, e.g., by hybridization to each other under stringent or under highly stringent conditions. Single stranded polynucleotides hybridize when they associate based on a variety of well characterized physical-chemical forces, such as hydrogen bonding, solvent exclusion, base stacking and the like. The stringency of a hybridization reflects the degree of sequence identity of the nucleic acids involved, such that the higher the stringency, the more similar are the two polynucleotide strands. Stringency is influenced by a variety of factors, including temperature, salt concentration and composition, organic and non-organic additives, solvents, etc. present in both the hybridization and wash solutions and incubations (and number thereof), as described in more detail in the references cited above. Encompassed by the invention are polynucleotide sequences that are capable of hybridizing to the claimed polynucleotide sequences, and, in particular, to those shown in SEQ ID NOs: 860; 802; 240; 274; 558; 24; 1120; 44; 460; 286; 120; 130; 134; 698; 832; 580; 612; 48, and fragments thereof under various conditions of stringency. (See, e.g., Wahl, G. M. and S. L. Berger (1987) Methods Enzymol. 152:399-407; Kimmel, A. R. (1987) Methods Enzymol. 152:507-511.) Estimates of homology are provided by either DNA-DNA or DNA-RNA hybridization under conditions of stringency as is well understood by those skilled in the art (Hames and Higgins, Eds. (1985) Nucleic Acid Hybridisation, IRL Press, Oxford, U.K.). Stringency conditions can be adjusted to screen for moderately similar fragments, such as homologous sequences from distantly related organisms, to highly similar fragments, such as genes that duplicate functional enzymes from closely related organisms. Post-hybridization washes determine stringency conditions.

In addition to the nucleotide sequences listed in Tables 4 and 5, full length cDNA, orthologs, paralogs and homologs of the present nucleotide sequences may be

identified and isolated using well known methods. The cDNA libraries orthologs, paralogs and homologs of the present nucleotide sequences may be screened using hybridization methods to determine their utility as hybridization target or amplification probes.

An example of stringent hybridization conditions for hybridization of complementary nucleic acids which have more than 100 complementary residues on a filter in a Southern or northern blot is about 5°C to 20°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH. The T_m is the temperature (under defined ionic strength and pH) at which 50% of the target sequence hybridizes to a perfectly matched probe. Nucleic acid molecules that hybridize under stringent conditions will typically hybridize to a probe based on either the entire cDNA or selected portions, e.g., to a unique subsequence, of the cDNA under wash conditions of 0.2x SSC to 2.0 x SSC, 0.1% SDS at 50-65° C. For example, high stringency is about 0.2 x SSC, 0.1% SDS at 65° C. Ultra-high stringency will be the same conditions except the wash temperature is raised about 3 to about 5° C, and ultra-ultra-high stringency will be the same conditions except the wash temperature is raised about 6 to about 9° C. For identification of less closely related homologues washes can be performed at a lower temperature, e.g., 50° C. In general, stringency is increased by raising the wash temperature and/or decreasing the concentration of SSC, as known in the art.

In another example, stringent salt concentration will ordinarily be less than about 750 mM NaCl and 75 mM trisodium citrate, preferably less than about 500 mM NaCl and 50 mM trisodium citrate, and most preferably less than about 250 mM NaCl and 25 mM trisodium citrate. Low stringency hybridization can be obtained in the absence of organic solvent, e.g., formamide, while high stringency hybridization can be obtained in the presence of at least about 35% formamide, and most preferably at least about 50% formamide. Stringent temperature conditions will ordinarily include temperatures of at least about 30° C, more preferably of at least about 37° C, and most preferably of at least about 42° C. Varying additional parameters, such as hybridization time, the concentration of detergent, e.g., sodium dodecyl sulfate (SDS), and the inclusion or exclusion of carrier DNA, are well known to those skilled in the

art. Various levels of stringency are accomplished by combining these various conditions as needed. In a preferred embodiment, hybridization will occur at 30° C in 750 mM NaCl, 75 mM trisodium citrate, and 1% SDS. In a more preferred embodiment, hybridization will occur at 37° C in 500 mM NaCl, 50 mM trisodium citrate, 1% SDS, 35% formamide, and 100 μg/ml denatured salmon sperm DNA (ssDNA). In a most preferred embodiment, hybridization will occur at 42° C in 250 mM NaCl, 25 mM trisodium citrate, 1% SDS, 50% formamide, and 200 μg/ml ssDNA. Useful variations on these conditions will be readily apparent to those skilled in the art.

The washing steps that follow hybridization can also vary in stringency. Wash stringency conditions can be defined by salt concentration and by temperature. As above, wash stringency can be increased by decreasing salt concentration or by increasing temperature. For example, stringent salt concentration for the wash steps will preferably be less than about 30 mM NaCl and 3 mM trisodium citrate, and most preferably less than about 15 mM NaCl and 1.5 mM trisodium citrate. Stringent temperature conditions for the wash steps will ordinarily include temperature of at least about 25° C, more preferably of at least about 42° C. Another preferred set of highly stringent conditions uses two final washes in 0.1X SSC, 0.1% SDS at 65° C. The most preferred high stringency washes are of at least about 68° C. For example, in a preferred embodiment, wash steps will occur at 25° C in 30 mM NaCl, 3 mM trisodium citrate, and 0.1% SDS. In a more preferred embodiment, wash steps will occur at 42° C in 15 mM NaCl, 1.5 mM trisodium citrate, and 0.1% SDS. In a most preferred embodiment, the wash steps will occur at 68° C in 15 mM NaCl, 1.5 mM trisodium citrate, and 0.1% SDS. Additional variations on these conditions will be readily apparent to those skilled in the art (see U.S. Patent Application No. 20010010913).

As another example, stringent conditions can be selected such that an oligonucleotide that is perfectly complementary to the coding oligonucleotide hybridizes to the coding oligonucleotide with at least about a 5-10x higher signal to noise ratio than the ratio for hybridization of the perfectly complementary oligonucleotide to a nucleic acid encoding a transcription factor known as of the filing

date of the application. Conditions can be selected such that a higher signal to noise ratio is observed in the particular assay which is used, e.g., about 15x, 25x, 35x, 50x or more. Accordingly, the subject nucleic acid hybridizes to the unique coding oligonucleotide with at least a 2x higher signal to noise ratio as compared to hybridization of the coding oligonucleotide to a nucleic acid encoding known polypeptide. Again, higher signal to noise ratios can be selected, e.g., about 5x, 10x, 25x, 35x, 50x or more. The particular signal will depend on the label used in the relevant assay, e.g., a fluorescent label, a colorimetric label, a radioactive label, or the like.

Alternatively, transcription factor homolog polypeptides can be obtained by screening an expression library using antibodies specific for one or more transcription factors. With the provision herein of the disclosed transcription factor, and transcription factor homologue nucleic acid sequences, the encoded polypeptide(s) can be expressed and purified in a heterologous expression system (e.g., *E. coli*) and used to raise antibodies (monoclonal or polyclonal) specific for the polypeptide(s) in question. Antibodies can also be raised against synthetic peptides derived from transcription factor, or transcription factor homologue, amino acid sequences. Methods of raising antibodies are well known in the art and are described in Harlow and Lane (1988) Antibodies: A Laboratory Manual, Cold Spring Harbor Laboratory, New York. Such antibodies can then be used to screen an expression library produced from the plant from which it is desired to clone additional transcription factor homologues, using the methods described above. The selected cDNAs can be confirmed by sequencing and enzymatic activity.

VII. Sequence Variations

It will readily be appreciated by those of skill in the art, that any of a variety of polynucleotide sequences are capable of encoding the transcription factors and transcription factor homologue polypeptides of the invention. Due to the degeneracy of the genetic code, many different polynucleotides can encode identical and/or substantially similar polypeptides in addition to those sequences illustrated in the Sequence Listing. Nucleic acids having a sequence that differs from the sequences shown in the Sequence Listing, or complementary sequences, that encode functionally equivalent peptides (i.e., peptides having some degree of equivalent or similar

biological activity) but differ in sequence from the sequence shown in the sequence listing due to degeneracy in the genetic code, are also within the scope of the invention.

Altered polynucleotide sequences encoding polypeptides include those sequences with deletions, insertions, or substitutions of different nucleotides, resulting in a polynucleotide encoding a polypeptide with at least one functional characteristic of the instant polypeptides. Included within this definition are polymorphisms which may or may not be readily detectable using a particular oligonucleotide probe of the polynucleotide encoding the instant polypeptides, and improper or unexpected hybridization to allelic variants, with a locus other than the normal chromosomal locus for the polynucleotide sequence encoding the instant polypeptides.

Allelic variant refers to any of two or more alternative forms of a gene occupying the same chromosomal locus. Allelic variation arises naturally through mutation, and may result in phenotypic polymorphism within populations. Gene mutations can be silent (i.e., no change in the encoded polypeptide) or may encode polypeptides having altered amino acid sequence. The term allelic variant is also used herein to denote a protein encoded by an allelic variant of a gene. Splice variant refers to alternative forms of RNA transcribed from a gene. Splice variation arises naturally through use of alternative splicing sites within a transcribed RNA molecule, or less commonly between separately transcribed RNA molecules, and may result in several mRNAs transcribed from the same gene. Splice variants may encode polypeptides having altered amino acid sequence. The term splice variant is also used herein to denote a protein encoded by a splice variant of an mRNA transcribed from a gene.

Those skilled in the art would recognize that the polypeptide sequence G681, SEQ ID NO: 580, represents a single transcription factor; allelic variation and alternative splicing may be expected to occur. Allelic variants of the polypeptide sequence of SEQ ID NO: 579 can be cloned by probing cDNA or genomic libraries from different individual organisms according to standard procedures. Allelic variants of the DNA sequence shown in SEQ ID NO: 579, including those containing silent mutations and those in which mutations result in amino acid sequence changes, are within the scope of the present invention, as are proteins which are allelic variants

of SEQ ID NO: 580. cDNAs generated from alternatively spliced mRNAs, which retain the properties of the transcription factor are included within the scope of the present invention, as are polypeptides encoded by such cDNAs and mRNAs. Allelic variants and splice variants of these sequences can be cloned by probing cDNA or genomic libraries from different individual organisms or tissues according to standard procedures known in the art (see USPN 6,388,064).

For example, Table 1 illustrates, e.g., that the codons AGC, AGT, TCA, TCC, TCG, and TCT all encode the same amino acid: serine. Accordingly, at each position in the sequence where there is a codon encoding serine, any of the above trinucleotide sequences can be used without altering the encoded polypeptide.

Table 1

Amino acid			Possible Codons					
Alanine	Ala	A	GCA	GCC	GCG	GCU		
Cysteine	Cys	C	TGC	TGT				
Aspartic acid	Asp	D	GAC	GAT				
Glutamic acid	Glu	E	GAA	GAG				
Phenylalanine	Phe	F	TTC	TTT				
Glycine	Gly	G	GGA	GGC	GGG	GGT		
Histidine	His	H	CAC	CAT				
Isoleucine	Ile	I	ATA	ATC	ATT			
Lysine	Lys	K	AAA	AAG				
Leucine	Leu	L	TTA	TTG	CTA	CTC	CTG	CTT
Methionine	Met	M	ATG					
Asparagine	Asn	N	AAC	AAT				
Proline	Pro	P	CCA	CCC	CCG	CCT		
Glutamine	Gln	Q	CAA	CAG				
Arginine	Arg	R	AGA	AGG	CGA	CGC	CGG	CGT
Serine	Ser	S	AGC	AGT	TCA	TCC	TCG	TCT
Threonine	Thr	T	ACA	ACC	ACG	ACT		
Valine	Val	V	GTA	GTC	GTG	GTT		
Tryptophan	Trp	W	TGG					
Tyrosine	Tyr	Y	TAC	TAT				

Sequence alterations that do not change the amino acid sequence encoded by the polynucleotide are termed "silent" variations. With the exception of the codons ATG and TGG, encoding methionine and tryptophan, respectively, any of the possible codons for the same amino acid can be substituted by a variety of techniques, e.g., site-directed mutagenesis, available in the art. Accordingly, any and all such variations of a sequence selected from the above table are a feature of the invention.

In addition to silent variations, other conservative variations that alter one, or a few amino acids in the encoded polypeptide, can be made without altering the function of the polypeptide, these conservative variants are, likewise, a feature of the invention.

For example, substitutions, deletions and insertions introduced into the sequences provided in the Sequence Listing are also envisioned by the invention. Such sequence modifications can be engineered into a sequence by site-directed mutagenesis (Wu (ed.) Meth. Enzymol. (1993) vol. 217, Academic Press) or the other methods noted below. Amino acid substitutions are typically of single residues; insertions usually will be on the order of about from 1 to 10 amino acid residues; and deletions will range about from 1 to 30 residues. In preferred embodiments, deletions or insertions are made in adjacent pairs, e.g., a deletion of two residues or insertion of two residues. Substitutions, deletions, insertions or any combination thereof can be combined to arrive at a sequence. The mutations that are made in the polynucleotide encoding the transcription factor should not place the sequence out of reading frame and should not create complementary regions that could produce secondary mRNA structure. Preferably, the polypeptide encoded by the DNA performs the desired function.

Conservative substitutions are those in which at least one residue in the amino acid sequence has been removed and a different residue inserted in its place. Such substitutions generally are made in accordance with the Table 2 when it is desired to maintain the activity of the protein. Table 2 shows amino acids which can be substituted for an amino acid in a protein and which are typically regarded as conservative substitutions.

Table 2

Residue	Conservative Substitutions
Ala	Ser
Arg	Lys
Asn	Gln; His
Asp	Glu
Gln	Asn
Cys	Ser
Glu	Asp
Gly	Pro
His	Asn; Gln
Ile	Leu, Val
Leu	Ile; Val
Lys	Arg; Gln
Met	Leu; Ile
Phe	Met; Leu; Tyr
Ser	Thr; Gly
Thr	Ser; Val
Trp	Tyr
Tyr	Trp; Phe
Val	Ile; Leu

Similar substitutions are those in which at least one residue in the amino acid sequence has been removed and a different residue inserted in its place. Such substitutions generally are made in accordance with the Table 3 when it is desired to maintain the activity of the protein. Table 3 shows amino acids which can be substituted for an amino acid in a protein and which are typically regarded as structural and functional substitutions. For example, a residue in column 1 of Table 3

may be substituted with residue in column 2; in addition, a residue in column 2 of Table 3 may be substituted with the residue of column 1.

Table 3

Residue	Similar Substitutions
Ala	Ser; Thr; Gly; Val; Leu; Ile
Arg	Lys; His; Gly
Asn	Gln; His; Gly; Ser; Thr
Asp	Glu, Ser; Thr
Gln	Asn; Ala
Cys	Ser; Gly
Glu	Asp
Gly	Pro; Arg
His	Asn; Gln; Tyr; Phe; Lys; Arg
Ile	Ala; Leu; Val; Gly; Met
Leu	Ala; Ile; Val; Gly; Met
Lys	Arg; His; Gln; Gly; Pro
Met	Leu; Ile; Phe
Phe	Met; Leu; Tyr; Trp; His; Val; Ala
Ser	Thr; Gly; Asp; Ala; Val; Ile; His
Thr	Ser; Val; Ala; Gly
Trp	Tyr; Phe; His
Tyr	Trp; Phe; His
Val	Ala; Ile; Leu; Gly; Thr; Ser; Glu

Substitutions that are less conservative than those in Table 2 can be selected by picking residues that differ more significantly in their effect on maintaining (a) the structure of the polypeptide backbone in the area of the substitution, for example, as a sheet or helical conformation, (b) the charge or hydrophobicity of the molecule at the target site, or (c) the bulk of the side chain. The substitutions which in general are

expected to produce the greatest changes in protein properties will be those in which (a) a hydrophilic residue, e.g., seryl or threonyl, is substituted for (or by) a hydrophobic residue, e.g., leucyl, isoleucyl, phenylalanyl, valyl or alanyl; (b) a cysteine or proline is substituted for (or by) any other residue; (c) a residue having an electropositive side chain, e.g., lysyl, arginyl, or histidyl, is substituted for (or by) an electronegative residue, e.g., glutamyl or aspartyl; or (d) a residue having a bulky side chain, e.g., phenylalanine, is substituted for (or by) one not having a side chain, e.g., glycine.

VIII. Further Modifying Sequences of the Invention – Mutation/Forced Evolution

In addition to generating silent or conservative substitutions as noted, above, the present invention optionally includes methods of modifying the sequences of the Sequence Listing. In the methods, nucleic acid or protein modification methods are used to alter the given sequences to produce new sequences and/or to chemically or enzymatically modify given sequences to change the properties of the nucleic acids or proteins.

Thus, in one embodiment, given nucleic acid sequences are modified, e.g., according to standard mutagenesis or artificial evolution methods to produce modified sequences. The modified sequences may be created using purified natural polynucleotides isolated from any organism or may be synthesized from purified compositions and chemicals using chemical means well know to those of skill in the art. For example, Ausubel, *supra*, provides additional details on mutagenesis methods. Artificial forced evolution methods are described, for example, by Stemmer (1994) Nature 370:389-391, Stemmer (1994) Proc. Natl. Acad. Sci. USA 91:10747-10751, and U.S. Patents 5,811,238, 5,837,500, and 6,242,568. Methods for engineering synthetic transcription factors and other polypeptides are described, for example, by Zhang et al. (2000) J. Biol. Chem. 275:33850-33860, Liu et al. (2001) J. Biol. Chem. 276:11323-11334, and Isalan et al. (2001) Nature Biotechnol. 19:656-660. Many other mutation and evolution methods are also available and expected to be within the skill of the practitioner.

Similarly, chemical or enzymatic alteration of expressed nucleic acids and polypeptides can be performed by standard methods. For example, sequence can be modified by addition of lipids, sugars, peptides, organic or inorganic compounds, by the inclusion of modified nucleotides or amino acids, or the like. For example, protein modification techniques are illustrated in Ausubel, *supra*. Further details on chemical and enzymatic modifications can be found herein. These modification methods can be used to modify any given sequence, or to modify any sequence produced by the various mutation and artificial evolution modification methods noted herein.

Accordingly, the invention provides for modification of any given nucleic acid by mutation, evolution, chemical or enzymatic modification, or other available methods, as well as for the products produced by practicing such methods, e.g., using the sequences herein as a starting substrate for the various modification approaches.

For example, optimized coding sequence containing codons preferred by a particular prokaryotic or eukaryotic host can be used e.g., to increase the rate of translation or to produce recombinant RNA transcripts having desirable properties, such as a longer half-life, as compared with transcripts produced using a non-optimized sequence. Translation stop codons can also be modified to reflect host preference. For example, preferred stop codons for *Saccharomyces cerevisiae* and mammals are TAA and TGA, respectively. The preferred stop codon for monocotyledonous plants is TGA, whereas insects and *E. coli* prefer to use TAA as the stop codon.

The polynucleotide sequences of the present invention can also be engineered in order to alter a coding sequence for a variety of reasons, including but not limited to, alterations which modify the sequence to facilitate cloning, processing and/or expression of the gene product. For example, alterations are optionally introduced using techniques which are well known in the art, e.g., site-directed mutagenesis, to insert new restriction sites, to alter glycosylation patterns, to change codon preference, to introduce splice sites, etc.

Furthermore, a fragment or domain derived from any of the polypeptides of the invention can be combined with domains derived from other transcription factors or synthetic domains to modify the biological activity of a transcription factor. For instance, a DNA-binding domain derived from a transcription factor of the invention can be combined with the activation domain of another transcription factor or with a synthetic activation domain. A transcription activation domain assists in initiating transcription from a DNA-binding site. Examples include the transcription activation region of VP16 or GAL4 (Moore et al. (1998) Proc. Natl. Acad. Sci. USA 95: 376-381; and Aoyama et al. (1995) Plant Cell 7:1773-1785), peptides derived from bacterial sequences (Ma and Ptashne (1987) Cell 51; 113-119) and synthetic peptides (Giniger and Ptashne, (1987) Nature 330:670-672).

IX. Expression and Modification of Polypeptides

Typically, polynucleotide sequences of the invention are incorporated into recombinant DNA (or RNA) molecules that direct expression of polypeptides of the invention in appropriate host cells, transgenic plants, in vitro translation systems, or the like. Due to the inherent degeneracy of the genetic code, nucleic acid sequences which encode substantially the same or a functionally equivalent amino acid sequence can be substituted for any listed sequence to provide for cloning and expressing the relevant homologue.

X. Vectors, Promoters, and Expression Systems

The present invention includes recombinant constructs comprising one or more of the nucleic acid sequences herein. The constructs typically comprise a vector, such as a plasmid, a cosmid, a phage, a virus (e.g., a plant virus), a bacterial artificial chromosome (BAC), a yeast artificial chromosome (YAC), or the like, into which a nucleic acid sequence of the invention has been inserted, in a forward or reverse orientation. In a preferred aspect of this embodiment, the construct further comprises regulatory sequences, including, for example, a promoter, operably linked to the sequence. Large numbers of suitable vectors and promoters are known to those of skill in the art, and are commercially available.

General texts that describe molecular biological techniques useful herein, including the use and production of vectors, promoters and many other relevant

topics, include Berger, Sambrook and Ausubel, *supra*. Any of the identified sequences can be incorporated into a cassette or vector, e.g., for expression in plants. A number of expression vectors suitable for stable transformation of plant cells or for the establishment of transgenic plants have been described including those described in Weissbach and Weissbach, (1989) Methods for Plant Molecular Biology, Academic Press, and Gelvin et al., (1990) Plant Molecular Biology Manual, Kluwer Academic Publishers. Specific examples include those derived from a Ti plasmid of *Agrobacterium tumefaciens*, as well as those disclosed by Herrera-Estrella et al. (1983) Nature 303: 209, Bevan (1984) Nucl Acid Res. 12: 8711-8721, Klee (1985) Bio/Technology 3: 637-642, for dicotyledonous plants.

Alternatively, non-Ti vectors can be used to transfer the DNA into monocotyledonous plants and cells by using free DNA delivery techniques. Such methods can involve, for example, the use of liposomes, electroporation, microprojectile bombardment, silicon carbide whiskers, and viruses. By using these methods transgenic plants such as wheat, rice (Christou (1991) Bio/Technology 9: 957-962) and corn (Gordon-Kamm (1990) Plant Cell 2: 603-618) can be produced. An immature embryo can also be a good target tissue for monocots for direct DNA delivery techniques by using the particle gun (Weeks et al. (1993) Plant Physiol 102: 1077-1084; Vasil (1993) Bio/Technology 10: 667-674; Wan and Lemeaux (1994) Plant Physiol 104: 37-48, and for *Agrobacterium*-mediated DNA transfer (Ishida et al. (1996) Nature Biotech 14: 745-750).

Typically, plant transformation vectors include one or more cloned plant coding sequence (genomic or cDNA) under the transcriptional control of 5' and 3' regulatory sequences and a dominant selectable marker. Such plant transformation vectors typically also contain a promoter (e.g., a regulatory region controlling inducible or constitutive, environmentally-or developmentally-regulated, or cell- or tissue-specific expression), a transcription initiation start site, an RNA processing signal (such as intron splice sites), a transcription termination site, and/or a polyadenylation signal.

Examples of constitutive plant promoters which can be useful for expressing the TF sequence include: the cauliflower mosaic virus (CaMV) 35S promoter, which

confers constitutive, high-level expression in most plant tissues (*see,* e.g., Odell et al. (1985) Nature 313:810-812); the nopaline synthase promoter (An et al. (1988) Plant Physiol 88:547-552); and the octopine synthase promoter (Fromm et al. (1989) Plant Cell 1: 977-984).

A variety of plant gene promoters that regulate gene expression in response to environmental, hormonal, chemical, developmental signals, and in a tissue-active manner can be used for expression of a TF sequence in plants. Choice of a promoter is based largely on the phenotype of interest and is determined by such factors as tissue (e.g., seed, fruit, root, pollen, vascular tissue, flower, carpel, etc.), inducibility (e.g., in response to wounding, heat, cold, drought, light, pathogens, etc.), timing, developmental stage, and the like. Numerous known promoters have been characterized and can favorably be employed to promote expression of a polynucleotide of the invention in a transgenic plant or cell of interest. For example, tissue specific promoters include: seed-specific promoters (such as the napin, phaseolin or DC3 promoter described in US Pat. No. 5,773,697), fruit-specific promoters that are active during fruit ripening (such as the dru 1 promoter (US Pat. No. 5,783,393), or the 2A11 promoter (US Pat. No. 4,943,674) and the tomato polygalacturonase promoter (Bird et al. (1988) Plant Mol Biol 11:651), root-specific promoters, such as those disclosed in US Patent Nos. 5,618,988, 5,837,848 and 5,905,186, pollen-active promoters such as PTA29, PTA26 and PTA13 (US Pat. No. 5,792,929), promoters active in vascular tissue (Ringli and Keller (1998) Plant Mol Biol 37:977-988), flower-specific (Kaiser et al, (1995) Plant Mol Biol 28:231-243), pollen (Baerson et al. (1994) Plant Mol Biol 26:1947-1959), carpels (Ohl et al. (1990) Plant Cell 2:837-848), pollen and ovules (Baerson et al. (1993) Plant Mol Biol 22:255-267), auxin-inducible promoters (such as that described in van der Kop et al. (1999) Plant Mol Biol 39:979-990 or Baumann et al. (1999) Plant Cell 11:323-334), cytokinin-inducible promoter (Guevara-Garcia (1998) Plant Mol Biol 38:743-753), promoters responsive to gibberellin (Shi et al. (1998) Plant Mol Biol 38:1053-1060, Willmott et al. (1998) 38:817-825) and the like. Additional promoters are those that elicit expression in response to heat (Ainley et al. (1993) Plant Mol Biol 22: 13-23), light (e.g., the pea rbcS-3A promoter, Kuhlemeier et al. (1989) Plant Cell 1:471, and the maize rbcS promoter, Schaffner and Sheen (1991) Plant Cell 3: 997); wounding (e.g., *wunI*, Siebertz et al. (1989) Plant Cell 1: 961); pathogens (such as the PR-1

promoter described in Buchel et al. (1999) Plant Mol. Biol. 40:387-396, and the PDF1.2 promoter described in Manners et al. (1998) Plant Mol. Biol. 38:1071-80), and chemicals such as methyl jasmonate or salicylic acid (Gatz et al. (1997) Plant Mol Biol 48: 89-108). In addition, the timing of the expression can be controlled by using promoters such as those acting at senescence (An and Amazon (1995) Science 270: 1986-1988); or late seed development (Odell et al. (1994) Plant Physiol 106:447-458).

Plant expression vectors can also include RNA processing signals that can be positioned within, upstream or downstream of the coding sequence. In addition, the expression vectors can include additional regulatory sequences from the 3'-untranslated region of plant genes, e.g., a 3' terminator region to increase mRNA stability of the mRNA, such as the PI-II terminator region of potato or the octopine or nopaline synthase 3' terminator regions.

Additional Expression Elements

Specific initiation signals can aid in efficient translation of coding sequences. These signals can include, e.g., the ATG initiation codon and adjacent sequences. In cases where a coding sequence, its initiation codon and upstream sequences are inserted into the appropriate expression vector, no additional translational control signals may be needed. However, in cases where only coding sequence (e.g., a mature protein coding sequence), or a portion thereof, is inserted, exogenous transcriptional control signals including the ATG initiation codon can be separately provided. The initiation codon is provided in the correct reading frame to facilitate transcription. Exogenous transcriptional elements and initiation codons can be of various origins, both natural and synthetic. The efficiency of expression can be enhanced by the inclusion of enhancers appropriate to the cell system in use.

Expression Hosts

The present invention also relates to host cells which are transduced with vectors of the invention, and the production of polypeptides of the invention (including fragments thereof) by recombinant techniques. Host cells are genetically engineered (i.e., nucleic acids are introduced, e.g., transduced, transformed or transfected) with the vectors of this invention, which may be, for example, a cloning vector or an expression vector comprising the relevant nucleic acids herein. The

vector is optionally a plasmid, a viral particle, a phage, a naked nucleic acid, *etc.* The engineered host cells can be cultured in conventional nutrient media modified as appropriate for activating promoters, selecting transformants, or amplifying the relevant gene. The culture conditions, such as temperature, pH and the like, are those previously used with the host cell selected for expression, and will be apparent to those skilled in the art and in the references cited herein, including, Sambrook and Ausubel.

The host cell can be a eukaryotic cell, such as a yeast cell, or a plant cell, or the host cell can be a prokaryotic cell, such as a bacterial cell. Plant protoplasts are also suitable for some applications. For example, the DNA fragments are introduced into plant tissues, cultured plant cells or plant protoplasts by standard methods including electroporation (Fromm et al., (1985) Proc. Natl. Acad. Sci. USA 82, 5824, infection by viral vectors such as cauliflower mosaic virus (CaMV) (Hohn et al., (1982) Molecular Biology of Plant Tumors, (Academic Press, New York) pp. 549-560; US 4,407,956), high velocity ballistic penetration by small particles with the nucleic acid either within the matrix of small beads or particles, or on the surface (Klein et al., (1987) Nature 327, 70-73), use of pollen as vector (WO 85/01856), or use of *Agrobacterium tumefaciens* or *A. rhizogenes* carrying a T-DNA plasmid in which DNA fragments are cloned. The T-DNA plasmid is transmitted to plant cells upon infection by *Agrobacterium tumefaciens*, and a portion is stably integrated into the plant genome (Horsch et al. (1984) Science 233:496-498; Fraley et al. (1983) Proc. Natl. Acad. Sci. USA 80, 4803).

The cell can include a nucleic acid of the invention which encodes a polypeptide, wherein the cells expresses a polypeptide of the invention. The cell can also include vector sequences, or the like. Furthermore, cells and transgenic plants that include any polypeptide or nucleic acid above or throughout this specification, e.g., produced by transduction of a vector of the invention, are an additional feature of the invention.

For long-term, high-yield production of recombinant proteins, stable expression can be used. Host cells transformed with a nucleotide sequence encoding a polypeptide of the invention are optionally cultured under conditions suitable for the

expression and recovery of the encoded protein from cell culture. The protein or fragment thereof produced by a recombinant cell may be secreted, membrane-bound, or contained intracellularly, depending on the sequence and/or the vector used. As will be understood by those of skill in the art, expression vectors containing polynucleotides encoding mature proteins of the invention can be designed with signal sequences which direct secretion of the mature polypeptides through a prokaryotic or eukaryotic cell membrane.

XI. Modified Amino Acid Residues

Polypeptides of the invention may contain one or more modified amino acid residues. The presence of modified amino acids may be advantageous in, for example, increasing polypeptide half-life, reducing polypeptide antigenicity or toxicity, increasing polypeptide storage stability, or the like. Amino acid residue(s) are modified, for example, co-translationally or post-translationally during recombinant production or modified by synthetic or chemical means.

Non-limiting examples of a modified amino acid residue include incorporation or other use of acetylated amino acids, glycosylated amino acids, sulfated amino acids, prenylated (e.g., farnesylated, geranylgeranylated) amino acids, PEG modified (e.g., "PEGylated") amino acids, biotinylated amino acids, carboxylated amino acids, phosphorylated amino acids, etc. References adequate to guide one of skill in the modification of amino acid residues are replete throughout the literature.

The modified amino acid residues may prevent or increase affinity of the polypeptide for another molecule, including, but not limited to, polynucleotide, proteins, carbohydrates, lipids and lipid derivatives, and other organic or synthetic compounds.

XII. Identification of Additional Factors

A transcription factor provided by the present invention can also be used to identify additional endogenous or exogenous molecules that can affect a phentoype or trait of interest. On the one hand, such molecules include organic (small or large molecules) and/or inorganic compounds that affect expression of (i.e., regulate) a particular transcription factor. Alternatively, such molecules include endogenous

molecules that are acted upon either at a transcriptional level by a transcription factor of the invention to modify a phenotype as desired. For example, the transcription factors can be employed to identify one or more downstream gene with which is subject to a regulatory effect of the transcription factor. In one approach, a transcription factor or transcription factor homologue of the invention is expressed in a host cell, e.g., a transgenic plant cell, tissue or explant, and expression products, either RNA or protein, of likely or random targets are monitored, e.g., by hybridization to a microarray of nucleic acid probes corresponding to genes expressed in a tissue or cell type of interest, by two-dimensional gel electrophoresis of protein products, or by any other method known in the art for assessing expression of gene products at the level of RNA or protein. Alternatively, a transcription factor of the invention can be used to identify promoter sequences (i.e., binding sites) involved in the regulation of a downstream target. After identifying a promoter sequence, interactions between the transcription factor and the promoter sequence can be modified by changing specific nucleotides in the promoter sequence or specific amino acids in the transcription factor that interact with the promoter sequence to alter a plant trait. Typically, transcription factor DNA-binding sites are identified by gel shift assays. After identifying the promoter regions, the promoter region sequences can be employed in double-stranded DNA arrays to identify molecules that affect the interactions of the transcription factors with their promoters (Bulyk et al. (1999) Nature Biotechnology 17:573-577).

The identified transcription factors are also useful to identify proteins that modify the activity of the transcription factor. Such modification can occur by covalent modification, such as by phosphorylation, or by protein-protein (homo or-heteropolymer) interactions. Any method suitable for detecting protein-protein interactions can be employed. Among the methods that can be employed are co-immunoprecipitation, cross-linking and co-purification through gradients or chromatographic columns, and the two-hybrid yeast system.

The two-hybrid system detects protein interactions in vivo and is described in Chien et al. ((1991), Proc. Natl. Acad. Sci. USA 88:9578-9582) and is commercially available from Clontech (Palo Alto, Calif.). In such a system, plasmids are constructed that encode two hybrid proteins: one consists of the DNA-binding domain

of a transcription activator protein fused to the TF polypeptide and the other consists of the transcription activator protein's activation domain fused to an unknown protein that is encoded by a cDNA that has been recombined into the plasmid as part of a cDNA library. The DNA-binding domain fusion plasmid and the cDNA library are transformed into a strain of the yeast *Saccharomyces cerevisiae* that contains a reporter gene (e.g., lacZ) whose regulatory region contains the transcription activator's binding site. Either hybrid protein alone cannot activate transcription of the reporter gene. Interaction of the two hybrid proteins reconstitutes the functional activator protein and results in expression of the reporter gene, which is detected by an assay for the reporter gene product. Then, the library plasmids responsible for reporter gene expression are isolated and sequenced to identify the proteins encoded by the library plasmids. After identifying proteins that interact with the transcription factors, assays for compounds that interfere with the TF protein-protein interactions can be preformed.

XIII. Identification of Modulators

In addition to the intracellular molecules described above, extracellular molecules that alter activity or expression of a transcription factor, either directly or indirectly, can be identified. For example, the methods can entail first placing a candidate molecule in contact with a plant or plant cell. The molecule can be introduced by topical administration, such as spraying or soaking of a plant, and then the molecule's effect on the expression or activity of the TF polypeptide or the expression of the polynucleotide monitored. Changes in the expression of the TF polypeptide can be monitored by use of polyclonal or monoclonal antibodies, gel electrophoresis or the like. Changes in the expression of the corresponding polynucleotide sequence can be detected by use of microarrays, Northerns, quantitative PCR, or any other technique for monitoring changes in mRNA expression. These techniques are exemplified in Ausubel et al. (eds) Current Protocols in Molecular Biology, John Wiley & Sons (1998, and supplements through 2001). Such changes in the expression levels can be correlated with modified plant traits and thus identified molecules can be useful for soaking or spraying on fruit, vegetable and grain crops to modify traits in plants.

Essentially any available composition can be tested for modulatory activity of expression or activity of any nucleic acid or polypeptide herein. Thus, available libraries of compounds such as chemicals, polypeptides, nucleic acids and the like can be tested for modulatory activity. Often, potential modulator compounds can be dissolved in aqueous or organic (e.g., DMSO-based) solutions for easy delivery to the cell or plant of interest in which the activity of the modulator is to be tested. Optionally, the assays are designed to screen large modulator composition libraries by automating the assay steps and providing compounds from any convenient source to assays, which are typically run in parallel (e.g., in microtiter formats on microtiter plates in robotic assays).

In one embodiment, high throughput screening methods involve providing a combinatorial library containing a large number of potential compounds (potential modulator compounds). Such "combinatorial chemical libraries" are then screened in one or more assays, as described herein, to identify those library members (particular chemical species or subclasses) that display a desired characteristic activity. The compounds thus identified can serve as target compounds.

A combinatorial chemical library can be, e.g., a collection of diverse chemical compounds generated by chemical synthesis or biological synthesis. For example, a combinatorial chemical library such as a polypeptide library is formed by combining a set of chemical building blocks (e.g., in one example, amino acids) in every possible way for a given compound length (i.e., the number of amino acids in a polypeptide compound of a set length). Exemplary libraries include peptide libraries, nucleic acid libraries, antibody libraries (see, e.g., Vaughn et al. (1996) Nature Biotechnology, 14(3):309-314 and PCT/US96/10287), carbohydrate libraries (see, e.g., Liang et al. Science (1996) 274:1520-1522 and U.S. Patent 5,593,853), peptide nucleic acid libraries (see, e.g., U.S. Patent 5,539,083), and small organic molecule libraries (see, e.g., benzodiazepines, Baum C&EN Jan 18, page 33 (1993); isoprenoids, U.S. Patent 5,569,588; thiazolidinones and metathiazanones, U.S. Patent 5,549,974; pyrrolidines, U.S. Patents 5,525,735 and 5,519,134; morpholino compounds, U.S. Patent 5,506,337) and the like.

Preparation and screening of combinatorial or other libraries is well known to those of skill in the art. Such combinatorial chemical libraries include, but are not limited to, peptide libraries (see, e.g., U.S. Patent 5,010,175; Furka, (1991) Int. J. Pept. Prot. Res. 37:487-493; and Houghton et al. (1991) Nature 354:84-88). Other chemistries for generating chemical diversity libraries can also be used.

In addition, as noted, compound screening equipment for high-throughput screening is generally available, e.g., using any of a number of well known robotic systems that have also been developed for solution phase chemistries useful in assay systems. These systems include automated workstations including an automated synthesis apparatus and robotic systems utilizing robotic arms. Any of the above devices are suitable for use with the present invention, e.g., for high-throughput screening of potential modulators. The nature and implementation of modifications to these devices (if any) so that they can operate as discussed herein will be apparent to persons skilled in the relevant art.

Indeed, entire high throughput screening systems are commercially available. These systems typically automate entire procedures including all sample and reagent pipetting, liquid dispensing, timed incubations, and final readings of the microplate in detector(s) appropriate for the assay. These configurable systems provide high throughput and rapid start up as well as a high degree of flexibility and customization. Similarly, microfluidic implementations of screening are also commercially available.

The manufacturers of such systems provide detailed protocols the various high throughput. Thus, for example, Zymark Corp. provides technical bulletins describing screening systems for detecting the modulation of gene transcription, ligand binding, and the like. The integrated systems herein, in addition to providing for sequence alignment and, optionally, synthesis of relevant nucleic acids, can include such screening apparatus to identify modulators that have an effect on one or more polynucleotides or polypeptides according to the present invention.

In some assays it is desirable to have positive controls to ensure that the components of the assays are working properly. At least two types of positive controls are appropriate. That is, known transcriptional activators or inhibitors can be

incubated with cells/plants/ etc. in one sample of the assay, and the resulting increase/decrease in transcription can be detected by measuring the resulting increase in RNA/ protein expression, etc., according to the methods herein. It will be appreciated that modulators can also be combined with transcriptional activators or inhibitors to find modulators that inhibit transcriptional activation or transcriptional repression. Either expression of the nucleic acids and proteins herein or any additional nucleic acids or proteins activated by the nucleic acids or proteins herein, or both, can be monitored.

In an embodiment, the invention provides a method for identifying compositions that modulate the activity or expression of a polynucleotide or polypeptide of the invention. For example, a test compound, whether a small or large molecule, is placed in contact with a cell, plant (or plant tissue or explant), or composition comprising the polynucleotide or polypeptide of interest and a resulting effect on the cell, plant, (or tissue or explant) or composition is evaluated by monitoring, either directly or indirectly, one or more of: expression level of the polynucleotide or polypeptide, activity (or modulation of the activity) of the polynucleotide or polypeptide. In some cases, an alteration in a plant phenotype can be detected following contact of a plant (or plant cell, or tissue or explant) with the putative modulator, e.g., by modulation of expression or activity of a polynucleotide or polypeptide of the invention. Modulation of expression or activity of a polynucleotide or polypeptide of the invention may also be caused by molecular elements in a signal transduction second messenger pathway and such modulation can affect similar elements in the same or another signal transduction second messenger pathway.

XIV. Subsequences

Also contemplated are uses of polynucleotides, also referred to herein as oligonucleotides, typically having at least 12 bases, preferably at least 15, more preferably at least 20, 30, or 50 bases, which hybridize under at least highly stringent (or ultra-high stringent or ultra-ultra-high stringent conditions) conditions to a polynucleotide sequence described above. The polynucleotides may be used as probes, primers, sense and antisense agents, and the like, according to methods as noted *supra*.

Subsequences of the polynucleotides of the invention, including polynucleotide fragments and oligonucleotides are useful as nucleic acid probes and primers. An oligonucleotide suitable for use as a probe or primer is at least about 15 nucleotides in length, more often at least about 18 nucleotides, often at least about 21 nucleotides, frequently at least about 30 nucleotides, or about 40 nucleotides, or more in length. A nucleic acid probe is useful in hybridization protocols, e.g., to identify additional polypeptide homologues of the invention, including protocols for microarray experiments. Primers can be annealed to a complementary target DNA strand by nucleic acid hybridization to form a hybrid between the primer and the target DNA strand, and then extended along the target DNA strand by a DNA polymerase enzyme. Primer pairs can be used for amplification of a nucleic acid sequence, e.g., by the polymerase chain reaction (PCR) or other nucleic-acid amplification methods. See Sambrook and Ausubel, *supra*.

In addition, the invention includes an isolated or recombinant polypeptide including a subsequence of at least about 15 contiguous amino acids encoded by the recombinant or isolated polynucleotides of the invention. For example, such polypeptides, or domains or fragments thereof, can be used as immunogens, e.g., to produce antibodies specific for the polypeptide sequence, or as probes for detecting a sequence of interest. A subsequence can range in size from about 15 amino acids in length up to and including the full length of the polypeptide.

To be encompassed by the present invention, an expressed polypeptide which comprises such a polypeptide subsequence performs at least one biological function of the intact polypeptide in substantially the same manner, or to a similar extent, as does the intact polypeptide. For example, a polypeptide fragment can comprise a recognizable structural motif or functional domain such as a DNA binding domain that binds to a specific DNA promoter region, an activation domain or a domain for protein-protein interactions.

XV. Production of Transgenic Plants

Modification of Traits

The polynucleotides of the invention are favorably employed to produce transgenic plants with various traits, or characteristics, that have been modified in a desirable manner, e.g., to improve the seed characteristics of a plant. For example, alteration of expression levels or patterns (e.g., spatial or temporal expression patterns) of one or more of the transcription factors (or transcription factor homologues) of the invention, as compared with the levels of the same protein found in a wild type plant, can be used to modify a plant's traits. An illustrative example of trait modification, improved characteristics, by altering expression levels of a particular transcription factor is described further in the Examples and the Sequence Listing.

Arabidopsis as a model system

Arabidopsis thaliana is the object of rapidly growing attention as a model for genetics and metabolism in plants. Arabidopsis has a small genome, and well documented studies are available. It is easy to grow in large numbers and mutants defining important genetically controlled mechanisms are either available, or can readily be obtained. Various methods to introduce and express isolated homologous genes are available (see Koncz, et al., eds. *Methods in Arabidopsis Research.* et al. (1992), World Scientific, New Jersey, New Jersey, in "Preface"). Because of its small size, short life cycle, obligate autogamy and high fertility, *Arabidopsis* is also a choice organism for the isolation of mutants and studies in morphogenetic and development pathways, and control of these pathways by transcription factors (Koncz, *supra*, p. 72). A number of studies introducing transcription factors into *A. thaliana* have demonstrated the utility of this plant for understanding the mechanisms of gene regulation and trait alteration in plants. See, for example, Koncz, *supra*, and U.S. Patent Number 6,417,428).

Arabidopsis genes in transgenic plants.

Expression of genes which encode transcription factors modify expression of endogenous genes, polynucleotides, and proteins are well known in the art. In addition, transgenic plants comprising isolated polynucleotides encoding transcription factors may also modify expression of endogenous genes, polynucleotides, and

proteins. Examples include Peng et al. (1997, Genes and Development 11:3194-3205) and Peng et al. (1999, Nature, 400:256-261). In addition, many others have demonstrated that an *Arabidopsis* transcription factor expressed in an exogenous plant species elicits the same or very similar phenotypic response. See, for example, Fu et al. (2001, Plant Cell 13:1791-1802); Nandi et al. (2000, Curr. Biol. 10:215-218); Coupland (1995, Nature 377:482-483); and Weigel and Nilsson (1995, Nature 377:482-500).

Homologous genes introduced into transgenic plants.

Homologous genes that may be derived from any plant, or from any source whether natural, synthetic, semi-synthetic or recombinant, and that share significant sequence identity or similarity to those provided by the present invention, may be introduced into plants, for example, crop plants, to confer desirable or improved traits. Consequently, transgenic plants may be produced that comprise a recombinant expression vector or cassette with a promoter operably linked to one or more sequences homologous to presently disclosed sequences. The promoter may be, for example, a plant or viral promoter.

The invention thus provides for methods for preparing transgenic plants, and for modifying plant traits. These methods include introducing into a plant a recombinant expression vector or cassette comprising a functional promoter operably linked to one or more sequences homologous to presently disclosed sequences. Plants and kits for producing these plants that result from the application of these methods are also encompassed by the present invention.

The complete descriptions of the traits associated with each polynucleotide of the invention is fully disclosed in Table 4, Table 5, and Table 6.

Table 4

Polynucleotide SEQ ID NO:	GID No.	Trait	Category	Family	Comment	Polypeptide SEQ ID NO:	Conserved domains
1	G1275	Architecture; size	Dev and morph	WRKY	Reduced apical dominance; small plant	2	(113-169)
3	G1411	Architecture	Dev and morph	AP2	Loss of apical dominance	4	(87-154)
5	G1488	Architecture; light response; size; seed protein content	Dev and morph; seed biochemistry	GATA/Zn	Reduced apical dominance, shorter stems; constitutive photomorphogenesis; reduced size; altered seed protein content	6	(221-246)
7	G1499	Architecture; flower; morphology: other	Dev and morph	HLH/MYC	Altered plant architecture; altered floral organ identity and development; dark green color	8	(118-181)
9	G1543	Architecture; flower; morphology: other; seed oil	Dev and morph; seed biochemistry	HB	Altered plant architecture; altered carpel shape; dark green color; decreased seed oil	10	(135-195)
11	G1635	Architecture; morphology: other; fertility	Dev and morph	MYB-related	Reduced apical dominance; pale green, smaller plants; reduced fertility	12	(44-104)
13	G1794	Architecture; light response; seed oil and protein content	Dev and morph; seed biochemistry	AP2	Altered plant architecture; constitutive photomorphogenesis; altered seed oil and protein content	14	(182-248)
15	G1839	Architecture; size	Dev and morph	AP2	Altered plant architecture; reduced size	16	(118-184)
17	G2108	Architecture	Dev and morph	AP2	Altered inflorescence structure	18	(18-85)
19	G2291	Architecture; flowering time	Dev and morph; flowering time	AP2	Altered plant architecture; late flowering	20	(TBD)
21	G2452	Architecture; leaf	Dev and morph	MYB-related	Reduced apical dominance; pale green color	22	(27-213)
23	G2509	Architecture; seed oil and protein content	Dev and morph; seed biochemistry	AP2	Reduced apical dominance; altered seed oil and protein content	24	(89-156)
25	G390	Architecture	Dev and morph	HB	Altered shoot development	26	(18-81)
27	G391	Architecture	Dev and morph	HB	Altered shoot development	28	(25-85)
29	G438	Architecture; stem	Dev and morph	HB	Reduced branching; reduced lignin	30	(22-85)

Table 4

31	G47	Architecture; stem; flowering time; altered seed oil content	Dev and morph; flowering time; seed biochemistry	AP2	Altered architecture and inflorescence development, structure of vascular tissues; late flowering; altered seed oil content	32	(11-80)
33	G559	Architecture; fertility	Dev and morph	bZIP	Loss of apical dominance; reduced fertility	34	(203-264)
35	G568	Architecture; flowering time	Dev and morph;	bZIP	Altered branching; late flowering	36	(215-265)
37	G580	Architecture; flower	Dev and morph	bZIP	Altered inflorescences; altered flower development	38	(162-218)
39	G615	Architecture; fertility	Dev and morph	TEO	Altered plant architecture; little or no pollen production, poor filament elongation	40	(88-147)
41	G732	Architecture; flower; seed oil and protein	Dev and morph; seed biochemistry	bZIP	Reduced apical dominance; abnormal flowers; altered seed oil and protein content	42	(31-91)
43	G988	Architecture; fertility; flower; stem; seed oil and protein content	Dev and morph; seed biochemistry	SCR	Reduced lateral branching; reduced fertility; enlarged floral organs, short pedicels; thicker stem, altered distribution of vacular bundles; altered seed oil and protein content	44	(178-195)
45	G1519	Embryo lethal	Dev and morph	RING/C3HC4	Embryo lethal	46	(327-364)
47	G374	Embryo lethal	Dev and morph	Z-ZPF	Embryo lethal	48	(35-67, 245-277)
49	G877	Embryo lethal	Dev and morph	WRKY	Embryo lethal	50	(272-328, 487-603)
51	G1000	Fertility; size; flower; stem	Dev and morph	MYB-(R1)R2R3	Reduced fertility; small plant; reduced or absent petals and sepals; reduced inflorescence, stem elongation	52	(14-117)
53	G1067	Fertility; leaf; size	Dev and morph	AT-hook	Reduced fertility; altered leaf shape; small plant	54	(86-93)
55	G1075	Fertility; flower; leaf; size	Dev and morph	AT-hook	Reduced fertility; reduced or absent petals, sepals and stamens; altered leaf shape; small plant	56	(78-85)
57	G1266	Fertility; size	Dev and morph	AP2	Reduced fertility; small plant	58	(79-147)
59	G1311	Fertility; size	Dev and morph	MYB-(R1)R2R3	Reduced fertility; small plant	60	(11-112)
61	G1321	Fertility; flower	Dev and morph	MYB-(R1)R2R3	Poor fertility; altered flower morphology	62	(4-106)
63	G1326	Fertility; flower; size	Dev and morph	MYB-(R1)R2R3	Reduced fertility; petals and sepals are smaller; small plant	64	(18-121)
65	G1367	Fertility; size	Dev and morph	AT-hook	Reduced fertility; reduced size	66	(179-201, 262-285, 298-319, 335-357)
67	G1386	Fertility; size; seed oil and protein content	Dev and morph; seed biochemistry	AP2	Reduced fertility; reduced size; altered seed oil and protein content	68	(TBD)

Table 4

69	G1421	Fertility; size; seed oil content	Dev and morph; seed biochemistry	AP2	Reduced fertility; small plant; altered seed oil content	70	(74-151)
71	G1453	Fertility; morphology: other	Dev and morph	NAC	Reduced fertility; altered inflorescence development	72	(13-160)
73	G1560	Fertility; flower; size	Dev and morph	HS	Reduced fertility; altered flower development; reduced size	74	(62-151)
75	G1594	Fertility; leaf; seed	Dev and morph	HB	Reduced fertility; altered leaf shape and development; large pale seed	76	(343-308)
77	G1750	Fertility; size; seed oil content	Dev and morph; seed biochemistry	AP2	Reduced fertility; reduced size; increased seed oil content	78	(107-173)
79	G1947	Fertility; flower; seed protein content	Dev and morph; seed biochemistry	HS	Reduced fertility; extended period of flowering; altered seed protein content	80	(37-120)
81	G2011	Fertility; size; seed oil and protein content	Dev and morph; seed biochemistry	HS	Reduced fertility; reduced size; altered seed oil and protein content	82	(56-147)
83	G2094	Fertility; leaf; size	Dev and morph	GATA/Zn	Reduced fertility; altered leaf development; reduced size	84	(43-68)
85	G2113	Fertility; leaf; seed protein content	Dev and morph; seed biochemistry	AP2	Reduced fertility; long petioles, altered orientation; altered seed protein content	86	(TBD)
87	G2115	Fertility; size	Dev and morph	AP2	Reduced fertility; reduced size	88	(46-115)
89	G2130	Fertility; size; senescence	Dev and morph	AP2	Reduced fertility; reduced size; early senescence	90	(93-160)
91	G2147	Fertility; size	Dev and morph	HLH/MYC	Reduced fertility; reduced size	92	(160-234)
93	G2156	Fertility; size; seed protein content	Dev and morph; seed biochemistry	AT-hook	Reduced fertility; reduced size; altered seed protein content	94	(66-86)
95	G2294	Fertility; size	Dev and morph	AP2	Reduced fertility; reduced size	96	(32-102)
97	G2510	Fertility; size	Dev and morph	AP2	Reduced fertility; reduced size	98	(41-108)
99	G2893	Fertility; flower; size	Dev and morph	MYB-(R1)R2R3	Reduced fertility; altered flower development; reduced size	100	(19-120)
101	G340	Fertility; size	Dev and morph	Z-C3H	Reduced fertility, size	102	(37-154)
103	G39	Fertility; size	Dev and morph	AP2	Reduced fertility, small plant	104	(24-90)
105	G439	Fertility; size	Dev and morph	AP2	Reduced fertility; small plant	106	(110-177)
107	G470	Fertility	Dev and morph	ARF	Short stamen filaments	108	(61-393)

Table 4

109	G652	Fertility; seed; flower; size; seed oil content	Dev and morph; seed biochemistry	Z-CLDSH	Reduced fertility; irregular shaped seed; altered flower development; reduced size, slow growth; altered seed oil content	110	(28-49, 137-151, 182-196)
111	G671	Fertility; flower; leaf; size; stem	Dev and morph	MYB-(R1)R2R3	Reduced fertility; reduced petal abscission; altered leaf shape; small plant; altered inflorescence stem structure	112	(15-115)
113	G779	Fertility; flower	Dev and morph	HLH/MYC	Reduced fertility, homeotic transformations	114	(126-182)
115	G962	Fertility; size	Dev and morph	NAC	Reduced fertility; small plant	116	(53-175)
117	G977	Fertility; leaf; morphology: other; size	Dev and morph	AP2	Reduced fertility; altered leaf shape; dark green; small plant	118	(5-72)
119	G1063	Flower; leaf; inflorescence; seed oil and protein content	Dev and morph; seed biochemistry	HLH/MYC	Altered flower development, ectopic carpel tissue; altered leaf shape, dark green color; altered inflorescence development; altered seed oil and protein content	120	(131-182)
121	G1140	Flower	Dev and morph	MADS	Altered flower development	122	(2-57)
123	G1425	Flower	Dev and morph	NAC	Altered flower and inflorescence development	124	(20-173)
125	G1449	Flower	Dev and morph	IAA	Altered flower structure	126	(48-53,74-107,122-152)
127	G1897	Flower; leaf; seed protein content	Dev and morph; seed biochemistry	Z-Dof	Altered flower development; altered leaf development; altered seed protein content	128	(34-62)
129	G2143	Flower; leaf; inflorescence	Dev and morph	HLH/MYC	Altered flower development, ectopic carpel tissue; altered leaf shape, dark green color; altered inflorescence development	130	(128-179)
131	G2535	Flower; seed protein content	Dev and morph; seed biochemistry	NAC	Altered flower development; altered seed protein content	132	(11-114)
133	G2557	Flower; leaf	Dev and morph	HLH/MYC	Altered flower development, ectopic carpel tissue; altered leaf shape, dark green color	134	(278-328)
135	G259	Flower; leaf	Dev and morph	HS	Altered flower development; altered leaf development	136	(27-131)
137	G353	Flower; leaf; size; seed protein content	Dev and morph; seed biochemistry	Z-C2H2	Short pedicels, downward pointing siliques; altered leaf development; reduced size; altered seed protein content	138	(41-61, 84-104)
139	G354	Flower; light response; size	Dev and morph	Z-C2H2	Short pedicels, downward pointing siliques; constitutive morphogenesis; reduced size	140	(42-62, 88-109)
141	G638	Flower; morphology: other	Dev and morph	TH	Altered flower development; multiple developmental defects	142	(119-206)

Table 4

143	G869	Flower; morphology: other; seed oil	Dev and morph; seed biochemistry	AP2	Abnormal anther development; small and spindly plant; altered seed fatty acids	144	(109-177)
145	G1645	Inflorescence; leaf	Dev and morph	MYB-(R1)R2R3	Altered inflorescence structure; altered leaf development	146	(90-210)
147	G1038	Leaf	Dev and morph	GARP	Altered leaf shape	148	(198-247)
149	G1073	Leaf; size; flowering time	Dev and morph; flowering time	AT-hook	Serrated leaves; increased plant size; flowering appears to be slightly delayed	150	(33-42, 78-175)
151	G1146	Leaf	Dev and morph	PAZ	Altered leaf development	152	(886-896)
153	G1267	Leaf; size	Dev and morph	WRKY	Dark green shiny leaves; small plant	154	(70-127)
155	G1269	Leaf	Dev and morph	MYB-related	Long petioles, upturned leaves	156	(27-83)
157	G1452	Leaf; trichome; flowering time	Dev and morph; flowering time	NAC	Altered leaf shape, dark green color; reduced trichome density; late flowering	158	(30-177)
159	G1494	Leaf; size; light response; seed	Dev and morph	HLH/MYC	Pale green leaves, altered leaf shape; reduced size; long hypocotyls; large, pale seeds	160	(261-311)
161	G1548	Leaf	Dev and morph	HB	Altered leaf development	162	(17-77)
163	G1574	Leaf	Dev and morph	SWI/SNF	Altered leaf development	164	(28-350)
165	G1586	Leaf; size	Dev and morph	HB	Narrow leaves; small plants	166	(21-81)
167	G1786	Leaf; light response; size	Dev and morph	MYB-(R1)R2R3	Dark green, small leaves with short petioles; photomorphogensis in the dark; small plant	168	(TBD)
169	G1792	Leaf; seed oil and protein content	Dev and morph; seed biochemistry	AP2	Dark green, shiny leaves; altered seed oil and protein content	170	(17-85)
171	G1865	Leaf; seed oil and protein content	Dev and morph; seed biochemistry	GRF-like	Altered leaf development; altered seed oil and protein content	172	(124-149)
173	G1886	Leaf; size	Dev and morph	Z-Dof	Chlorotic patches in leaves; reduced size	174	(17-59)
175	G1933	Leaf; size; seed protein content	Dev and morph; seed biochemistry	WRKY	Altered leaf development; reduced size; altered seed protein content	176	(205-263, 344-404)
177	G2059	Leaf; seed oil and protein content	Dev and morph; seed biochemistry	AP2	Smaller, curled leaves; altered seed oil, protein content	178	(184-254)
179	G2105	Leaf; seed	Dev and morph	TH	Alterations in leaf surface; large, pale seeds	180	(100-153)
181	G2117	Leaf; seed oil and protein content	Dev and morph; seed biochemistry	bZIP	Small, dark green leaves; altered seed oil and protein content	182	(46-106)

Table 4

183	G2124	Leaf; seed protein content	Dev and morph; seed biochemistry	TEO	Altered leaf development; altered seed protein content	184	(75-132)
185	G2140	Leaf; root	Dev and morph	HLH/MYC	Altered leaf development; short roots	186	(167-242)
187	G2144	Leaf; light response; size; seed oil content	Dev and morph; seed biochemistry	HLH/MYC	Pale green leaves, altered leaf shape; long hypocotyls; reduced size; altered seed oil content	188	(203-283)
189	G2431	Leaf	Dev and morph	GARP	Dark green leaves; reduced size	190	(38-88)
191	G2465	Morphology: other; leaf	Dev and morph	GARP	Slowed development; altered leaf color and shape	192	(219-269)
193	G2583	Leaf; seed oil and protein content	Dev and morph; seed biochemistry	AP2	Glossy, shiny leaves; altered seed oil and protein content	194	(4-71)
195	G2724	Leaf	Dev and morph	MYB-(R1)R2R3	Dark green leaves	196	(7-113)
197	G377	Leaf; morphology: other	Dev and morph	RING/C3H2C3	Altered leaf development; slow growth	198	(85-128)
199	G428	Leaf	Dev and morph	HB	Altered leaf shape	200	(229-292)
201	G447	Leaf; morphology: other; size	Dev and morph	ARF	Dark green leaves; altered cotyledon shape; reduced size	202	(22-356)
203	G464	Leaf	Dev and morph	IAA	Altered leaf shape	204	(20-28, 71-82, 126-142, 187-224)
205	G557	Leaf; size	Dev and morph	bZIP	Dark green color; small plant	206	(90-150)
207	G577	Leaf	Dev and morph	BZIPT2	Reduced size, increased anthocyanins	208	(TBD)
209	G674	Leaf; size	Dev and morph	MYB-(R1)R2R3	Dark green leaves, upwardly oriented; reduced size	210	(20-120)
211	G736	Leaf; flowering time	Dev and morph; flowering time	Z-Dof	Altered leaf shape; later flowering	212	(54-111)
213	G903	Leaf	Dev and morph	Z-C2H2	Altered leaf morphology	214	(68-92)
215	G917	Leaf; seed oil and protein content	Dev and morph; seed biochemistry	MADS	Altered leaf development; altered seed oil and protein content	216	(2-57)
217	G921	Leaf	Dev and morph	WRKY	Serrated leaves	218	(146-203)
219	G922	Leaf; size	Dev and morph	SCR	Altered development, dark green color; reduced size	220	(225-242)
221	G932	Leaf; size	Dev and morph	MYB-(R1)R2R3	Altered development, dark green color; reduced size	222	(12-118)
223	G599	Leaf; size	Dev and morph	DBP	Altered leaf shape; small plant	224	(187-219, 264-300)
225	G804	Leaf; size	Dev and morph	PCF	Altered leaf shape, small plant	226	(54-117)

Table 4

227	G1062	Light response; morphology; other; seed	Dev and morph	HLH/MYC	Constitutive photomorphogenesis; slow growth; altered seed shape	228	(308-359)
229	G1322	Light response; size	Dev and morph	MYB-(R1)R2R3	Photomorphogenesis in the dark; reduced size	230	(26-130)
231	G1331	Light response; morphology: other; seed oil and protein content	Dev and morph; seed biochemistry	MYB-(R1)R2R3	Constitutive photomorphogenesis; multiple developmental alterations; altered seed oil and protein content	232	(8-109)
233	G1521	Light response	Dev and morph	RING/C3HC4	Constitutive photomorphogenesis	234	(39-80)
235	G183	Light response; seed protein content	Dev and morph; seed biochemistry	WRKY	Constitutive photomorphogenesis; altered seed protein content	236	(307-363)
237	G2555	Light response	Dev and morph	HLH/MYC	Constitutive photomorphogenesis	238	(175-245)
239	G375	Light response	Dev and morph	Z-Dof	Upward pointing leaves	240	(75-103)
241	G1007	Morphology: other	Dev and morph	AP2	Multiple developmental alterations	242	(TBD)
243	G1010	Morphology: other	Dev and morph	ABI3/VP-1	Multiple developmental alterations	244	(33-122)
245	G1014	Morphology: other; trichome	Dev and morph	ABI3/VP-1	Multiple developmental defects; reduced trichomes	246	(90-172)
247	G1035	Morphology: other	Dev and morph	bZIP	Multiple developmental alterations	248	(39-91)
249	G1046	Morphology: other	Dev and morph	bZIP	Multiple developmental alterations	250	(79-138)
251	G1049	Morphology: other; seed protein content	Dev and morph; seed biochemistry	bZIP	Multiple developmental alterations; altered seed protein content	252	(77-132)
253	G1069	Morphology: other; seed oil content	Dev and morph; seed biochemistry	AT-hook	Multiple developmental alterations; altered seed oil content	254	(67-74)
255	G1070	Morphology: other	Dev and morph	AT-hook	Several developmental defects	256	(98-120)
257	G1076	Morphology: other	Dev and morph	AT-hook	Lethal when overexpressed	258	(82-89)
259	G1089	Morphology: other	Dev and morph	BZIPT2	Developmental defects at seedling stage	260	(425-500)
261	G1093	Morphology: other	Dev and morph	RING/C3H2C3	Multiple morphological alterations	262	(105-148)

Table 4

263	G1127	Morphology: other	Dev and morph	AT-hook	Multiple developmental alterations	264	(103-110, 155-162)
265	G1131	Morphology: other; seed protein content	Dev and morph; seed biochemistry	HLH/MYC	Multiple developmental alterations; altered seed protein content	266	(173-220)
267	G1145	Morphology: other; seed oil and protein	Dev and morph; seed biochemistry	bZIP	Multiple developmental alterations; reduced seed size, altered seed shape; altered seed oil and protein content	268	(227-270)
269	G1229	Morphology: other; seed oil and protein content	Dev and morph; seed biochemistry	HLH/MYC	Several developmental defects; altered seed oil and protein content	270	(102-160)
271	G1246	Morphology: other; seed protein content	Dev and morph; seed biochemistry	MYB-(R1)R2R3	Multiple developmental alterations; altered seed protein content	272	(27-139)
273	G1255	Morphology: other; seed	Dev and morph	Z-CO-like	Reduced apical dominance; increased seed size	274	(18-56)
275	G1304	Morphology: other	Dev and morph	MYB-(R1)R2R3	Lethal when overexpressed	276	(13-118)
277	G1318	Morphology: other	Dev and morph	MYB-(R1)R2R3	Multiple developmental alterations	278	(20-123)
279	G1320	Morphology: other	Dev and morph	MYB-(R1)R2R3	Multiple developmental alterations	280	(5-108)
281	G1330	Morphology: other	Dev and morph	MYB-(R1)R2R3	Multiple developmental alterations	282	(28-134)
283	G1352	Morphology: other	Dev and morph	Z-C2H2	Multiple developmental alterations	284	(108-129,167-188)
285	G1354	Morphology: other	Dev and morph	NAC	Multiple developmental alterations	286	(TBD)
287	G1360	Morphology: other	Dev and morph	NAC	Lethal when overexpressed	288	(18-174)
289	G1364	Morphology: other	Dev and morph	CAAT	Lethal when overexpressed	290	(29-120)
291	G1379	Morphology: other	Dev and morph	AP2	Multiple developmental alterations	292	(18-85)
293	G1384	Morphology: other	Dev and morph	AP2	Abnormal inflorescence and flower development	294	(TBD)
295	G1399	Morphology: other	Dev and morph	AT-hook	Multiple developmental alterations	296	(86-93)

Table 4

297	G1415	Morphology: other	Dev and morph	AP2	Multiple developmental alterations	298	(TBD)
299	G1417	Morphology: other; seed oil	Dev and morph; seed biochemistry	WRKY	Reduced seedling germination and vigor; increase in 18:2, decrease in 18:3	300	(239-296)
301	G1442	Morphology: other	Dev and morph	GRF-like	Multiple developmental alterations	302	(172-223)
303	G1454	Morphology: other; seed oil and protein content	Dev and morph; seed biochemistry	NAC	Multiple developmental alterations; altered seed oil and protein content	304	(9-178)
305	G1459	Morphology: other	Dev and morph	NAC	Multiple developmental alterations	306	(10-152)
307	G1460	Morphology: other; seed protein content	Dev and morph; seed biochemistry	NAC	Multiple developmental alterations; altered seed protein content	308	(TBD)
309	G147	Morphology: other	Dev and morph	MADS	Multiple developmental defects	310	(2-57)
311	G1471	Morphology: other; seed oil	Dev and morph; seed biochemistry	Z-C2H2	Multiple developmental alterations; increased seed oil content	312	(49-70)
313	G1475	Morphology: other	Dev and morph	Z-C2H2	Multiple developmental alterations	314	(51-73)
315	G1477	Morphology: other	Dev and morph	Z-C2H2	Multiple developmental alterations	316	(29-48)
317	G1487	Morphology: other; seed oil and protein content	Dev and morph: seed biochemistry	GATA/Zn	Multiple developmental alterations; altered seed oil and protein content	318	(251-276)
319	G1492	Morphology: other	Dev and morph	GARP	Multiple developmental alterations	320	(34-83)
321	G1531	Morphology: other; seed; seed protein content	Dev and morph; seed biochemistry	RING/C3HC4	Multiple developmental alterations; pale seed; altered seed protein content	322	(41-77)
323	G1540	Morphology: other	Dev and morph	HB	Reduced cell differentiation in meristem	324	(35-98)
325	G1544	Morphology: other	Dev and morph	HB	Multiple developmental alterations	326	(64-124)

Table 4

327	G156	Morphology: other; seed	Dev and morph	MADS	Multiple developmental defects; seed color alteration	328	(2-57)
329	G1584	Morphology: other	Dev and morph	HB	Multiple developmental alterations	330	(TBD)
331	G1587	Morphology: other	Dev and morph	HB	Multiple developmental alterations	332	(61-121)
333	G1588	Morphology: other	Dev and morph	HB	Multiple developmental alterations	334	(66-124)
335	G1589	Morphology: other; seed protein content	Dev and morph; seed biochemistry	HB	Multiple developmental alterations; altered seed protein content	336	(384-448)
337	G160	Morphology: other	Dev and morph	MADS	Multiple developmental defects	338	(7-62)
339	G1636	Morphology: other	Dev and morph	MYB-related	Pale green, smaller plants	340	(100-165)
341	G1642	Morphology: other	Dev and morph	MYB-(R1)R2R3	Multiple developmental alterations	342	(TBD)
343	G1747	Morphology: other; seed protein content	Dev and morph; seed biochemistry	MYB-(R1)R2R3	Multiple developmental alterations; altered seed protein content	344	(11-114)
345	G1749	Morphology: other	Dev and morph	AP2	Multiple developmental alterations; formation of necrotic lesions	346	(84-155)
347	G1751	Morphology: other	Dev and morph	AP2	Multiple developmental alterations	348	(TBD)
349	G1752	Morphology: other	Dev and morph	AP2	Multiple developmental alterations	350	(83-151)
351	G1763	Morphology: other	Dev and morph	AP2	Lethal when overexpressed	352	(140-209)
353	G1766	Morphology: other	Dev and morph	NAC	Multiple developmental alterations	354	(10-153)
355	G1767	Morphology: other; seed oil content	Dev and morph; seed biochemistry	SCR	Multiple developmental alterations; altered seed oil content	356	(255-272)
357	G1778	Morphology: other	Dev and morph	GATA/Zn	Lethal when overexpressed	358	(94-119)
359	G1789	Morphology: other; seed protein content	Dev and morph; seed biochemistry	MYB-related	Delayed development; altered seed protein content	360	(1-50)
361	G1790	Morphology: other	Dev and morph	MYB-(R1)R2R3	Lethal when overexpressed	362	(217-316)

Table 4

363	G1791	Morphology: other	Dev and morph	AP2	Multiple developmental alterations	364	(TBD)
365	G1793	Morphology: other; seed oil	Dev and morph; seed biochemistry	AP2	Multiple developmental alterations; increased seed oil content	366	(179-255, 281-349)
367	G1795	Morphology: other; trichome	Dev and morph	AP2	Multiple developmental alterations; reduced trichomes	368	(12-80)
369	G1800	Morphology: other	Dev and morph	AP2	Multiple developmental alterations	370	(TBD)
371	G1806	Morphology: other	Dev and morph	bZIP	Multiple developmental alterations	372	(165-225)
373	G1811	Morphology: other	Dev and morph	ABI3/VP-1	Multiple developmental alterations	374	(TBD)
375	G182	Morphology: other	Dev and morph	WRKY	Multiple developmental alterations	376	(217-276)
377	G1835	Morphology: other	Dev and morph	GATA/Zn	Small, spindly plant	378	(224-296)
379	G1836	Morphology: other	Dev and morph	CAAT	Pale green	380	(30-164)
381	G1838	Morphology: other; seed oil content	Dev and morph; seed biochemistry	AP2	Multiple developmental alterations; increased seed oil content	382	(229-305, 330-400)
383	G1843	Morphology: other	Dev and morph	MADS	Multiple developmental alterations	384	(2-57)
385	G1853	Morphology: other	Dev and morph	AKR	Lethal when overexpressed	386	(entire protein)
387	G1855	Morphology: other	Dev and morph	AKR	Slow growth	388	(entire protein)
389	G187	Morphology: other	Dev and morph	WRKY	Variety of morphological alterations	390	(172-228)
391	G1881	Morphology: other	Dev and morph	Z-CO-like	Multiple developmental alterations	392	(5-28, 56-79)
393	G1882	Morphology: other	Dev and morph	Z-Dof	Lethal when overexpressed	394	(97-125)
395	G1883	Morphology: other	Dev and morph	Z-Dof	Multiple developmental alterations	396	(82-124)
397	G1884	Morphology: other	Dev and morph	Z-Dof	Multiple developmental alterations	398	(43-71)
399	G1891	Morphology: other	Dev and morph	Z-Dof	Multiple developmental alterations	400	(27-69)

Table 4

401	G1896	Morphology: other	Dev and morph	Z-Dof	Multiple developmental alterations	402	(43-85)
403	G1898	Morphology: other	Dev and morph	Z-Dof	Lethal when overexpressed	404	(31-59)
405	G1902	Morphology: other; seed oil content	Dev and morph; seed biochemistry	Z-Dof	Multiple developmental alterations; increased seed oil content	406	(31-59)
407	G1904	Morphology: other	Dev and morph	Z-Dof	Multiple developmental alterations	408	(53-95)
409	G1906	Morphology: other	Dev and morph	Z-Dof	Multiple developmental alterations	410	(19-47)
411	G1913	Morphology: other	Dev and morph	Z-Dof	Lethal when overexpressed	412	(27-55)
413	G1914	Morphology: other	Dev and morph	Z-C2H2	Multiple developmental alterations	414	(195-216, 245-266)
415	G1925	Morphology: other	Dev and morph	NAC	Multiple developmental alterations	416	(6-150)
417	G1929	Morphology: other	Dev and morph	Z-CO-like	Slow growth, delayed development	418	(31-53)
419	G1930	Morphology: other	Dev and morph	AP2	Multiple developmental alterations	420	(59-124)
421	G195	Morphology: other	Dev and morph	WRKY	Multiple developmental defects	422	(183-239)
423	G1954	Morphology: other	Dev and morph	HLH/MYC	Lethal when overexpressed	424	(187-259)
425	G1958	Morphology: other; seed protein content	Dev and morph; seed biochemistry	GARP	Reduced size and root mass in plates.; altered seed protein content	426	(230-278)
427	G196	Morphology: other; seed protein content	Dev and morph; seed biochemistry	WRKY	Multiple developmental alterations; altered seed protein content	428	(223-283)
429	G1965	Morphology: other	Dev and morph	Z-Dof	Lethal when overexpressed	430	(27-55)
431	G1976	Morphology: other	Dev and morph	Z-C2H2	Multiple developmental alterations	432	(219-323)
433	G2057	Morphology: other	Dev and morph	TEO	Multiple developmental alterations	434	(TBD)
435	G2107	Morphology: other	Dev and morph	AP2	Multiple developmental alterations	436	(TBD)

Table 4

437	G211	Morphology: other	Dev and morph	MYB-(R1)R2R3	Multiple developmental alterations	438	(24-137)
439	G2133	Morphology: other; flowering time; seed protein content	Dev and morph; flowering time	AP2	Multiple developmental alterations; late flowering; altered seed protein content	440	(11-83)
441	G2134	Morphology: other	Dev and morph	AP2	Multiple developmental alterations	442	(TBD)
443	G2151	Morphology: other; seed oil and protein content	Dev and morph; seed biochemistry	AT-hook	Multiple developmental alterations; altered seed oil and protein content	444	(93-113, 124-144)
445	G2154	Morphology: other	Dev and morph	AT-hook	Multiple developmental alterations	446	(97-119)
447	G2157	Morphology: other	Dev and morph	AT-hook	Multiple developmental alterations	448	(82-102, 164-107)
449	G2181	Morphology: other	Dev and morph	NAC	Multiple developmental alterations	450	(22-169)
451	G221	Morphology: other	Dev and morph	MYB-(R1)R2R3	Multiple developmental alterations	452	(21-125)
453	G2290	Morphology: other	Dev and morph	WRKY	Multiple developmental alterations	454	(147-205)
455	G2299	Morphology: other	Dev and morph	AP2	Multiple developmental alterations	456	(48-115)
457	G2340	Morphology: other; seed oil and protein content	Dev and morph; seed biochemistry	MYB-(R1)R2R3	Tissue necrosis; multiple developmental alterations; altered seed oil and protein content	458	(14-120)
459	G2346	Morphology: other	Dev and morph	SBP	Enlarged seedlings	460	(59-135)
461	G237	Morphology: other	Dev and morph	MYB-(R1)R2R3	Multiple developmental alterations	462	(11-113)
463	G2373	Morphology: other; seed protein content	Dev and morph; seed biochemistry	TH	Multiple developmental alterations; altered seed protein content	464	(290-350)
465	G2376	Morphology: other; seed oil protein	Dev and morph; seed biochemistry	TH	Seedling lethality; altered seed protein content	466	(79-178, 336-408)
467	G24	Morphology: other	Dev and morph	AP2	Reduced size and necrotic patches	468	(25-93)

Table 4

469	G2424	Morphology: other	Dev and morph	MYB-(R1)R2R3	Multiple developmental alterations	470	(107-219)
471	G2505	Morphology: other	Dev and morph	NAC	Lethal when overexpressed	472	(10-159)
473	G2512	Morphology: other	Dev and morph	AP2	Multiple developmental alterations	474	(79-139)
475	G2513	Morphology: other	Dev and morph	AP2	Multiple developmental alterations	476	(TBD)
477	G2519	Morphology: other	Dev and morph	HLH/MYC	Multiple developmental alterations	478	(1-65)
479	G2520	Morphology: other; seed oil and protein content	Dev and morph; seed biochemistry	HLH/MYC	Multiple developmental alterations; altered seed oil and protein content	480	(135-206)
481	G2533	Morphology: other; seed protein content	Dev and morph; seed biochemistry	NAC	Multiple developmental alterations; altered seed protein content	482	(11-186)
483	G2534	Morphology: other	Dev and morph	NAC	Lethal when overexpressed	484	(10-157)
485	G2573	Morphology: other; seed oil and protein content	Dev and morph; seed biochemistry	AP2	Multiple developmental alterations; altered seed oil and protein content	486	(31-98)
487	G2589	Morphology: other	Dev and morph	MADS	Multiple developmental alterations	488	(2-57)
489	G2687	Morphology: other	Dev and morph	AP2	Multiple developmental alterations	490	(51-120)
491	G27	Morphology: other	Dev and morph	AP2	Abnormal development, small	492	(37-104)
493	G2720	Morphology: other; seed oil and protein content	Dev and morph; seed biochemistry	MYB-(R1)R2R3	Multiple developmental alterations; altered seed oil and protein content	494	(10-114)
495	G2787	Morphology: other; seed oil content	Dev and morph; seed biochemistry	AT-hook	Multiple developmental alterations; altered seed oil content	496	(172-192, 226-247, 256-276, 290-311, 245-366)
497	G2789	Morphology: other	Dev and morph	AT-hook	Multiple developmental alterations	498	(53-73, 121-165)
499	G31	Morphology: other	Dev and morph	AP2	Multiple developmental alterations	500	(TBD)

Table 4

501	G33	Morphology: other	Dev and morph	AP2	Multiple developmental defects	502	(50-117)
503	G342	Morphology: other; seed oil and protein content	Dev and morph; seed biochemistry	GATA/Zn	Multiple developmental alterations; altered seed oil and protein content	504	(155-190)
505	G352	Morphology: other	Dev and morph	Z-C2H2	Multiple developmental alterations	506	(99-119,166-186)
507	G357	Morphology: other	Dev and morph	Z-C2H2	Developmental defect	508	(7-29)
509	G358	Morphology: other	Dev and morph	Z-C2H2	Lethal when overexpressed	510	(124-135, 188-210)
511	G360	Morphology: other	Dev and morph	Z-C2H2	Multiple developmental alterations	512	(42-62)
513	G362	Size; Morphology: other; trichome; flowering time; seed protein content	Dev and morph; flowering time; seed biochemistry	Z-C2H2	Reduced size; increased pigmentation in seed, embryos and other organs; ectopic trichome formation; increased trichome number; late flowering; altered protein content	514	(62-82)
515	G364	Morphology: other	Dev and morph	Z-C2H2	Developmental defect	516	(54-76)
517	G365	Morphology: other	Dev and morph	Z-C2H2	Multiple developmental alterations	518	(70-90)
519	G367	Morphology: other	Dev and morph	Z-C2H2	Lethal when overexpressed	520	(63-84)
521	G373	Morphology: other	Dev and morph	RING/C3HC4	Multiple developmental alterations	522	(129-168)
523	G396	Morphology: other; size	Dev and morph	HB	Altered leaf coloration and shape, reduced fertility; small plant	524	(159-220)
525	G431	Morphology: other	Dev and morph	HB	Developmental defect, sterile	526	(286-335)
527	G479	Morphology: other	Dev and morph	SBP	Multiple developmental alterations	528	(70-149)
529	G546	Morphology: other	Dev and morph	RING/C3H2C3	Slow growth and development; increased anthocyanin pigmentation	530	(114-155)
531	G551	Morphology: other	Dev and morph	HB	Multiple developmental alterations	532	(73-133)
533	G578	Morphology: other	Dev and morph	bZIP	Lethal when overexpressed	534	(36-96)

Table 4

535	G596	Morphology: other	Dev and morph	AT-hook	Multiple developmental alterations	536	(89-96)
537	G617	Morphology: other	Dev and morph	TEO	Multiple developmental alterations	538	(64-118)
539	G620	Morphology: other; seed protein content	Dev and morph; seed biochemistry	CAAT	Multiple developmental alterations; altered seed protein content	540	(20-118)
541	G625	Morphology: other	Dev and morph	AP2	Lethal when overexpressed	542	(52-119)
543	G658	Morphology: other	Dev and morph	MYB-(R1)R2R3	Developmental defect	544	(2-105)
545	G716	Morphology: other	Dev and morph	ARF	Multiple developmental defects	546	(24-355)
547	G725	Morphology: other	Dev and morph	GARP	Developmental defect	548	(39-87)
549	G727	Morphology: other	Dev and morph	GARP	Multiple morphological alterations	550	(226-269)
551	G740	Morphology: other	Dev and morph	Z-CLDSH	Slow growth	552	(24-42, 232-268)
553	G770	Morphology: other	Dev and morph	NAC	Multiple developmental alterations	554	(19-162)
555	G858	Morphology: other	Dev and morph	MADS	Multiple developmental alterations	556	(2-57)
557	G865	Morphology: other; seed protein content	Dev and morph; seed biochemistry	AP2	Altered morphology; increased seed protein	558	(36-103)
559	G872	Morphology: other	Dev and morph	AP2	Multiple developmental alterations	560	(18-85)
561	G904	Morphology: other	Dev and morph	RING/C3H2C3	Multiple developmental alterations	562	(117-158)
563	G910	Morphology: other; flowering time	Dev and morph; flowering time	Z-CO-like	Multiple developmental alterations; late flowering	564	(14-37, 77-103)
565	G912	Morphology: other; size; sugar sensing; flowering time	Dev and morph; sugar sensing; flowering time	AP2	Dark green color; small plant; reduced cotyledon expansion in glucose; late flowering	566	(51-118)
567	G920	Morphology: other	Dev and morph	WRKY	Multiple developmental alterations	568	(152-211)

Table 4

569	G939	Morphology: other; size	Dev and morph	EIL	Pale seedlings on agar; reduced size	570	(97-106)
571	G963	Morphology: other; seed protein content	Dev and morph; seed biochemistry	NAC	Slowed growth rate; altered seed protein content	572	(TBD)
573	G979	Morphology: other; seed	Dev and morph	AP2	Several developmental defects; altered seed development, ripening and germination	574	(63-139,165-233)
575	G987	Morphology: other	Dev and morph	SCR	Developmental defects	576	(428-432,704-708)
577	G993	Morphology: other; seed protein content	Dev and morph; seed biochemistry	AP2	Multiple developmental alterations; altered seed protein content	578	(69-134)
579	G681	Morphology: other; leaf glucosinolates	Dev and morph; leaf biochemistry	MYB-(R1)R2R3	Multiple developmental alterations; overexpression results in an increase in M39480	580	(14-120)
581	G1482	Root	Dev and morph	Z-CO-like	Increased root growth	582	(5-63)
583	G225	Root; trichome	Dev and morph	MYB-related	Increased root hairs; glabrous, lack of trichomes	584	(39-76)
585	G226	Root; trichome; seed protein content	Dev and morph; seed biochemistry	MYB-related	Increased root hairs; glabrous, lack of trichomes; increased seed protein	586	(28-78)
587	G9	Root	Dev and morph	AP2	Increased root mass	588	(62-127)
589	G1040	Seed	Dev and morph	GARP	Smaller and more rounded seeds	590	(109-158)
591	G2114	Seed	Dev and morph	AP2	Increased seed size	592	(221-297, 323-393)
593	G450	Seed; size; seed protein content	Dev and morph; seed biochemistry	IAA	Increased seed size; reduced plant size; altered seed protein content	594	(TBD)
595	G584	Seed	Dev and morph	HLH/MYC	Large seeds	596	(401-494)
597	G668	Seed	Dev and morph	MYB-(R1)R2R3	Reduced seed color	598	(13-113)
599	G1050	Senescence	Dev and morph	bZIP	Delayed senescence	600	(372-425)
601	G1463	Senescence	Dev and morph	NAC	Premature senescence	602	(9-156)
603	G1944	Senescence; size; seed protein content	Dev and morph; seed biochemistry	AT-hook	Early senescence; reduced size; altered seed protein content	604	(87-100)
605	G2383	Senescence; seed protein content	Dev and morph; seed biochemistry	TEO	Early senescence; altered seed protein content	606	(89-149)
607	G571	Senescence; flowering time	Dev and morph; flowering time	bZIP	Delayed senescence; late flowering	608	(160-220)

Table 4

609	G636	Senescence; size	Dev and morph	TH	Premature senescence; reduced size	610	(55-145, 405-498)
611	G878	Senescence; flowering time	Dev and morph; flowering time	WRKY	Delayed senescence; late flowering	612	(250-305, 415-475)
613	G1134	Silique	Dev and morph	HLH/MYC	Siliques with altered shape	614	(198-247)
615	G1008	Size	Dev and morph	AP2	Small plant	616	(96-163)
617	G1020	Size	Dev and morph	AP2	Very small T1 plants	618	(28-95)
619	G1023	Size	Dev and morph	AP2	Reduced size	620	(128-195)
621	G1053	Size	Dev and morph	bZIP	Small plant	622	(74-120)
623	G1137	Size	Dev and morph	HLH/MYC	Small T1 plants	624	(264-314)
625	G1181	Size	Dev and morph	HS	Small T1 plants	626	(24-114)
627	G1228	Size	Dev and morph	HLH/MYC	Reduced size	628	(179-233)
629	G1277	Size	Dev and morph	AP2	Small plant	630	(18-85)
631	G1309	Size	Dev and morph	MYB-(R1)R2R3	Small plant	632	(9-114)
633	G1314	Size; sugar sensing; seed protein content	Dev and morph; sugar sensing; seed biochemistry	MYB-(R1)R2R3	Reduced size; reduced seedling vigor on high glucose; altered seed protein content	634	(14-116)
635	G1317	Size	Dev and morph	MYB-(R1)R2R3	Reduced size	636	(13-118)
637	G1323	Size; seed oil and protein content	Dev and morph; seed biochemistry	MYB-(R1)R2R3	Small T1 plants, dark green; decreased seed oil, increased seed protein	638	(15-116)
639	G1332	Size; trichome; seed oil and protein content	Dev and morph; seed biochemistry	MYB-(R1)R2R3	Reduced size; reduced trichome density; altered seed oil and protein content	640	(13-116)
641	G1334	Size	Dev and morph	CAAT	Small, dark green	642	(18-190)
643	G1381	Size	Dev and morph	AP2	Reduced size	644	(68-135)
645	G1382	Size	Dev and morph	WRKY	Small plant	646	(210-266, 385-437)
647	G1435	Size; flowering time	Dev and morph; flowering time	GARP	Increased plant size; late flowering	648	(146-194)
649	G1537	Size	Dev and morph	HB	Small T1 plants with altered development	650	(14-74)
651	G1545	Size	Dev and morph	HB	Reduced size	652	(54-117)
653	G1641	Size; seed oil and protein content	Dev and morph; seed biochemistry	MYB-related	Small plant; altered seed oil and protein content	654	(139-200)
655	G165	Size; seed protein content	Dev and morph; seed biochemistry	MADS	Reduced size; altered seed protein content	656	(7-62)

Table 4

657	G1652	Size; seed oil and protein content	Dev and morph; seed biochemistry	HLH/MYC	Reduced size; altered seed oil and protein content	658	(143-215)
659	G1655	Size	Dev and morph	HLH/MYC	Small plant	660	(134-192)
661	G1671	Size	Dev and morph	NAC	Reduced size	662	(TBD)
663	G1756	Size; seed protein content	Dev and morph; seed biochemistry	WRKY	Reduced size; altered seed protein content	664	(TBD)
665	G1757	Size; seed protein content	Dev and morph; seed biochemistry	WRKY	Small plant; altered seed protein content	666	(158-218)
667	G1782	Size	Dev and morph	CAAT	Small, spindly plant	668	(166-238)
669	G184	Size	Dev and morph	WRKY	Small plant	670	(295-352)
671	G1845	Size	Dev and morph	AP2	Small plant	672	(140-207)
673	G1879	Size; seed oil and protein content	Dev and morph; seed biochemistry	HLH/MYC	Reduced size; altered seed oil and protein content	674	(107-176)
675	G1888	Size	Dev and morph	Z-CO-like	Reduced size, dark green leaves	676	(5-50)
677	G189	Size; seed protein content	Dev and morph; seed biochemistry	WRKY	Increased leaf size; altered seed protein content	678	(240-297)
679	G1939	Size	Dev and morph	PCF	Reduced size	680	(40-102)
681	G194	Size	Dev and morph	WRKY	Small plant	682	(174-230)
683	G1943	Size	Dev and morph	HLH/MYC	Reduced size	684	(335-406)
685	G21	Size; seed oil and protein content	Dev and morph; seed biochemistry	AP2	Reduced size; altered seed oil and protein content	686	(97-164)
687	G2132	Size; seed oil and protein content	Dev and morph; seed biochemistry	AP2	Reduced size; altered seed oil and protein content	688	(TBD)
689	G2145	Size	Dev and morph	HLH/MYC	Reduced size	690	(166-243)
691	G23	Size	Dev and morph	AP2	Small T1 plants	692	(61-117)
693	G2313	Size	Dev and morph	MYB-related	Reduced size	694	(TBD)
695	G2344	Size	Dev and morph	CAAT	Reduced size, slow growth	696	(TBD)
697	G2430	Size	Dev and morph	GARP	Increased leaf size, faster development	698	(425-478)
699	G2517	Size	Dev and morph	WRKY	Reduced size	700	(118-234)
701	G2521	Size	Dev and morph	HLH/MYC	Reduced size	702	(145-213)
703	G258	Size; seed oil and protein content	Dev and morph; seed biochemistry	MYB-(R1)R2R3	Reduced size; altered seed oil and protein content	704	(24-124)

Table 4

705	G280	Size; seed protein content	Dev and morph; seed biochemistry	AT-hook	Reduced size; altered seed protein content	706	(97-104,130-137-155-162,185-192)
707	G3	Size	Dev and morph	AP2	Small plant	708	(28-95)
709	G343	Size	Dev and morph	GATA/Zn	Small plant	710	(178-214)
711	G363	Size	Dev and morph	Z-C2H2	Small plant	712	(87-108)
713	G370	Size	Dev and morph	Z-C2H2	Reduced size, shiny leaves	714	(97-117)
715	G385	Size	Dev and morph	HB	Small plant, short inflorescence stems, dark green	716	(60-123)
717	G439	Size	Dev and morph	AP2	Small plant	718	(110-177)
719	G440	Size	Dev and morph	AP2	Small plant	720	(122-189)
721	G5	Size	Dev and morph	AP2	Small plant	722	(149-216)
723	G550	Size	Dev and morph	Z-Dof	Small plant	724	(134-180)
725	G670	Size	Dev and morph	MYB-(R1)R2R3	Small plant	726	(14-122)
727	G760	Size	Dev and morph	NAC	Reduced size	728	(12-156)
729	G831	Size	Dev and morph	AKR	Reduced size	730	(470-591)
731	G864	Size	Dev and morph	AP2	Small plant	732	(119-186)
733	G884	Size	Dev and morph	WRKY	Reduced size	734	(227-285, 407-465)
735	G898	Size; seed oil and protein content	Dev and morph; seed biochemistry	RING/C3HC4	Reduced size; altered seed oil and protein content	736	(148-185)
737	G900	Size	Dev and morph	Z-CO-like	Reduced size	738	(6-28, 48-74)
739	G913	Size; flowering time	Dev and morph; flowering time	AP2	Small plant; late flowering	740	(62-128)
741	G937	Size	Dev and morph	GARP	Slightly reduced size	742	(197-246)
743	G960	Size	Dev and morph	NAC	Small plant	744	(13-156)
745	G991	Size; seed oil and protein content	Dev and morph; seed biochemistry	IAA	Slightly reduced size; altered seed oil and protein content	746	(7-14,48-59,82-115,128-164)
747	G748	Stem; flowering time	Dev and morph; flowering time	Z-Dof	More vascular bundles in stem; late flowering	748	(112-140)
749	G247	Trichome; seed protein content	Dev and morph; seed biochemistry	MYB-(R1)R2R3	Altered trichome distribution; altered seed protein content	750	(15-116)
751	G585	Trichome	Dev and morph	HLH/MYC	Reduced trichome density	752	(436-501)
753	G634	Trichome; seed protein content	Dev and morph; seed biochemistry	TH	Increased trichome density and size; altered seed protein content	754	(62-147, 189-245)
755	G676	Trichome	Dev and morph	MYB-(R1)R2R3	Reduced trichomes	756	(17-119)

Table 4

757	G682	Trichome	Dev and morph	MYB-related	Glabrous, lack of trichomes	758	(27-63)
759	G635	Variegation	Dev and morph	TH		760	(239-323)
761	G1068	Sugar sensing	Sugar sensing	AT-hook	Reduced cotyledon expansion in glucose	762	(143-150)
763	G1225	Sugar sensing; seed oil and protein content	Sugar sensing; seed biochemistry	HLH/MYC	Better germination on sucrose and glucose media; altered seed oil and protein content	764	(78-147)
765	G1337	Sugar sensing	Sugar sensing	Z-CO-like	Decreased germination on sucrose medium	766	(9-75)
767	G1759	Sugar sensing	Sugar sensing	MADS	Reduced germination on high glucose	768	(2-57)
769	G1804	Sugar sensing; flowering time	Sugar sensing; flowering time	bZIP	Altered sugar sensing; late flowering	770	(357-407)
771	G207	Sugar sensing	Sugar sensing	MYB-(R1)R2R3	Decreased germination on glucose medium	772	(6-106)
773	G218	Sugar sensing; seed oil content	Sugar sensing; seed biochemistry	MYB-(R1)R2R3	Reduced cotyledon expansion in glucose; altered seed oil content	774	(TBD)
775	G241	Sugar sensing; seed oil and protein content	Sugar sensing; seed biochemistry	MYB-(R1)R2R3	Decreased germination and growth on glucose medium; decreased seed oil, altered protein content	776	(14-114)
777	G254	Sugar sensing	Sugar sensing	MYB-related	Decreased germination and growth on glucose medium	778	(62-106)
779	G26	Sugar sensing	Sugar sensing	AP2	Decreased germination and growth on glucose medium	780	(67-134)
781	G263	Sugar sensing	Sugar sensing	HS	Decreased root growth on sucrose medium, root specific expression	782	(TBD)
783	G308	Sugar sensing	Sugar sensing	SCR	No germination on glucose medium	784	(270-274)
785	G38	Sugar sensing	Sugar sensing	AP2	Reduced germination on glucose medium	786	(76-143)
787	G43	Sugar sensing	Sugar sensing	AP2	Decreased germination and growth on glucose medium	788	(104-172)
789	G536	Sugar sensing	Sugar sensing	GF14	Decreased germination and growth on glucose medium	790	(226-233)
791	G567	Sugar sensing; seed oil and protein content	Sugar sensing; seed biochemistry	bZIP	Decreased seedling vigor on high glucose; altered seed oil and protein content	792	(210-270)
793	G680	Sugar sensing; flowering time	Sugar sensing; flowering time	MYB-related	Reduced germination on glucose medium; late flowering	794	(24-70)
795	G867	Sugar sensing	Sugar sensing	AP2	Better seedling vigor on sucrose medium	796	(59-124)
797	G956	Sugar sensing	Sugar sensing	NAC	Reduced germination on glucose medium	798	(TBD)
799	G996	Sugar sensing	Sugar sensing	MYB-(R1)R2R3	Reduced germination on glucose medium	800	(14-114)
801	G1946	Seed glucosinolates, oil, protein content	Seed biochemistry	HS	Increase in M3950; increased oil content; decreased protein content	802	(32-130)
803	G217	Seed oil composition	Seed biochemistry	MYB-related	Increase in 20:2	804	(8-67)

Table 4

805	G2192	Seed oil composition	Seed biochemistry	bZIP-NIN	Altered composition	806	(600-700)
807	G504	Seed oil composition;	Seed biochemistry	NAC	Altered seed oil composition and content; altered seed protein content	808	(TBD)
809	G622	Seed oil composition	Seed biochemistry	ABI3/VP-1	Decreased 18:2 fatty acid	810	(TBD)
811	G778	Seed oil composition	Seed biochemistry	HLH/MYC	Increased seed 18:1 fatty acid	812	(220-267)
813	G791	Seed oil composition	Seed biochemistry	HLH/MYC	Altered seed fatty acid composition	814	(75-143)
815	G861	Seed oil composition; seed oil content	Seed biochemistry	MADS	Increase in 16:1; altered seed oil content	816	(2-57)
817	G938	Seed oil composition	Seed biochemistry	EIL	Altered seed fatty acid composition	818	(96-104)
819	G965	Seed oil composition	Seed biochemistry	HB	Increase in 18:1	820	(423-486)
821	G1143	Seed oil and protein content	Seed biochemistry	HLH/MYC	Altered seed oil and protein content	822	(33-82)
823	G1190	Seed oil content	Seed biochemistry	AKR	Increased content	824	(entire protein)
825	G1198	Seed oil and protein content	Seed biochemistry	bZIP	Altered seed oil and protein content	826	(173-223)
827	G1226	Seed oil and protein content	Seed biochemistry	HLH/MYC	Altered seed oil and protein content	828	(115-174)
829	G1451	Seed oil content	Seed biochemistry	ARF	Altered seed oil content	830	(22-357)
831	G1478	Seed oil and protein content; flowering time	Seed biochemistry; flowering time	Z-CO-like	Altered seed oil, protein content; late flowering	832	(32-76)
833	G1496	Seed oil content	Seed biochemistry	HLH/MYC	Altered seed oil content	834	(184-248)
835	G1526	Seed oil content	Seed biochemistry	SWI/SNF	Increased seed oil content	836	(493-620, 864-1006)
837	G1543	Seed oil content	Seed biochemistry	HB	Decreased seed oil	838	(135-195)
839	G162	Seed oil and protein content	Seed biochemistry	MADS	Altered seed oil content; altered seed oil and protein content	840	(2-57)

Table 4

841	G1640	Seed oil content	Seed biochemistry	MYB-(R1)R2R3	Increased seed oil	842	(14-115)
843	G1644	Seed oil and protein content	Seed biochemistry	MYB-(R1)R2R3	Altered seed oil, protein content	844	(39-102)
845	G1646	Seed oil content	Seed biochemistry	CAAT	Altered seed oil content	846	(72-162)
847	G1672	Seed oil content	Seed biochemistry	NAC	Altered seed oil content	848	(41-194)
849	G1677	Seed oil and protein content	Seed biochemistry	NAC	Altered seed oil, protein content	850	(17-181)
851	G1765	Seed oil and protein content	Seed biochemistry	NAC	Altered seed oil and protein content	852	(20-140)
853	G1777	Seed oil and protein content	Seed biochemistry	RING/C3HC4	Increased oil, decreased protein content	854	(124-247)
855	G1793	Seed oil content	Seed biochemistry	AP2	Increased seed oil content	856	(179-255, 281-349)
857	G180	Seed oil content	Seed biochemistry	WRKY	Decreased seed oil content	858	(118-174)
859	G192	Seed oil and protein content; flowering time	Seed biochemistry; flowering time	WRKY	Altered seed oil and protein content; late flowering	860	(128-185)
861	G1948	Seed oil and protein content	Seed biochemistry	AKR	Altered seed oil and protein content	862	(entire protein)
863	G2123	Seed oil and protein content	Seed biochemistry	GF14	Altered seed oil and protein content	864	(99-109)
865	G2138	Seed oil content	Seed biochemistry	AP2	Increased seed oil content	866	(TBD)
867	G2139	Seed oil content	Seed biochemistry	MADS	Increased seed content	868	(14-69)
869	G2343	Seed oil content	Seed biochemistry	MYB-(R1)R2R3	Altered seed oil content	870	(14-116)
871	G265	Seed oil and protein content	Seed biochemistry	HS	Altered seed oil and protein content	872	(11-105)
873	G2792	Seed oil content	Seed biochemistry	HLH/MYC	Increased seed oil content	874	(190-258)
875	G2830	Seed oil and protein content	Seed biochemistry	Z-C2H2	Altered seed oil and protein content	876	(245-266)
877	G286	Seed oil and protein content	Seed biochemistry	ENBP	Altered seed oil and protein content	878	(TBD)

Table 4

879	G291	Seed oil content	Seed biochemistry	MISC	Increased seed oil content	880	(132-160)
881	G427	Seed oil and protein content	Seed biochemistry	HB	Increased oil content; decreased protein content	882	(307-370)
883	G509	Seed oil and protein content	Seed biochemistry	NAC	Altered seed oil and protein content	884	(13-169)
885	G519	Seed oil and protein content	Seed biochemistry	NAC	Altered seed oil and protein content	886	(11-104)
887	G561	Seed oil content	Seed biochemistry	bZIP	Altered seed oil content	888	(248-308)
889	G590	Seed oil and protein content	Seed biochemistry	HLH/MYC	Altered seed oil and protein content	890	(202-254)
891	G818	Seed oil content	Seed biochemistry	HS	Increased content	892	(70-162)
893	G849	Seed oil and protein content	Seed biochemistry	BPF-1	Increased seed oil, altered protein content	894	(324-413, 504-583)
895	G892	Seed oil and protein content	Seed biochemistry	RING/C3H2C3	Altered seed oil, protein content	896	(177-270)
897	G961	Seed oil content	Seed biochemistry	NAC	Altered seed oil content	898	(15-140)
899	G1465	Seed oil and protein content	Seed biochemistry	NAC	Altered seed oil and protein content	900	(242-306)
901	G425	Seed oil content	Seed biochemistry	HB	Altered seed oil content	902	(TBD)
903	G347	Seed oil and protein content	Seed biochemistry	Z-LSDlike	Altered seed oil and protein content	904	(9-39, 50-70, 80-127)
905	G1512	Seed oil and protein content	Seed biochemistry	RING/C3HC4	Altered seed oil and protein content	906	(39-93)
907	G2069	Seed oil and protein content	Seed biochemistry	bZIP	Altered seed oil and protein content	908	(TBD)
909	G1852	Seed oil content	Seed biochemistry	AKR	Altered seed oil content	910	(1-601)
911	G1793	Seed oil content	Seed biochemistry	AP2	Altered seed oil content	912	(179-255, 281-349)
913	G761	Seed oil and protein content	Seed biochemistry	NAC	Altered seed oil and protein content	914	(10-156)
915	G1056	Seed oil content	Seed biochemistry	bZIP	Altered seed oil content	916	(183-246)
917	G1447	Seed oil content	Seed biochemistry	MISC	Altered seed oil content	918	(3-54, 124-156)

Table 4

919	G323	Seed oil and protein content	Seed biochemistry	RING/C3HC4	Altered seed oil and protein content	920	(48-96)
921	G176	Seed oil content	Seed biochemistry	WRKY	Altered seed oil content	922	(117-173,234-290)
923	G174	Seed oil and protein content	Seed biochemistry	WRKY	Altered seed oil and protein content	924	(111-166, 283-339)
925	G715	Seed oil content	Seed biochemistry	CAAT	Altered seed oil content	926	(60-132)
927	G588	Seed oil and protein content	Seed biochemistry	HLH/MYC	Altered seed oil and protein content	928	(309-376)
929	G1758	Seed oil and protein content	Seed biochemistry	WRKY	Altered seed oil and protein content	930	(109-165)
931	G2148	Seed oil content	Seed biochemistry	HLH/MYC	Altered seed oil content	932	(130-268)
933	G2379	Seed oil content	Seed biochemistry	TH	Altered seed oil content	934	(19-110, 173-232)
935	G1462	Seed oil content	Seed biochemistry	NAC	Altered seed oil content	936	(TBD)
937	G1211	Seed oil and protein content	Seed biochemistry	MISC	Altered seed oil and protein content	938	(123-179)
939	G1048	Seed oil content	Seed biochemistry	bZIP	Altered seed oil content	940	(138-190)
941	G986	Seed oil content	Seed biochemistry	WRKY	Altered seed oil content	942	(146-203)
943	G789	Seed oil content	Seed biochemistry	HLH/MYC	Altered seed oil content	944	(253-313)
945	G2085	Seed oil and protein content	Seed biochemistry	RING/C3HC4	Altered seed oil and protein content	946	(TBD)
947	G1783	Seed oil and protein content	Seed biochemistry	MYB-related	Altered seed oil and protein content	948	(81..129)
949	G2072	Seed oil and protein content	Seed biochemistry	bZIP	Altered seed oil and protein content	950	(90-149)
951	G931	Seed oil and protein content	Seed biochemistry	CAAT	Altered seed oil and protein content	952	(TBD)
953	G278	Seed oil and protein content	Seed biochemistry	AKR	Altered seed oil and protein content	954	(2-593)
955	G2421	Seed oil content	Seed biochemistry	MYB-(R1)R2R3	Altered seed oil content	956	(9-110)
957	G2032	Seed oil content	Seed biochemistry	AKR	Altered seed oil content	958	(entire protein)

Table 4

959	G1396	Seed oil and protein content	Seed biochemistry	S1FA	Altered seed oil and protein content	960	(TBD)
961	G619	Seed oil and protein content	Seed biochemistry	ARF	Altered seed oil and protein content	962	(64-406)
963	G2295	Seed oil content	Seed biochemistry	MADS	Altered seed oil content	964	(2-57)
965	G312	Seed oil content	Seed biochemistry	SCR	Altered seed oil content	966	(320-336)
967	G1444	Seed oil and protein content	Seed biochemistry	GRF-like	Altered seed oil and protein content	968	(168-193)
969	G801	Seed oil content	Seed biochemistry	PCF	Altered seed oil content	970	(32-93)
971	G1950	Seed oil content	Seed biochemistry	AKR	Altered seed oil content	972	(65-228)
973	G958	Seed oil and protein content	Seed biochemistry	NAC	Altered seed oil and protein content	974	(7-156)
975	G1037	Seed oil and protein content	Seed biochemistry	GARP	Altered seed oil and protein content	976	(11-134, 200-248)
977	G2065	Seed oil content	Seed biochemistry	MADS	Altered seed oil content	978	(TBD)
979	G2137	Seed oil and protein content	Seed biochemistry	WRKY	Altered seed oil and protein content	980	(109-168)
981	G746	Seed oil content	Seed biochemistry	RING/C3HC4	Altered seed oil content	982	(139-178)
983	G2701	Seed oil and protein content	Seed biochemistry	MYB-related	Altered seed oil and protein content	984	(33-81, 129-183)
985	G1819	Seed oil content	Seed biochemistry	CAAT	Altered seed oil content	986	(46-188)
987	G1227	Seed oil and protein content	Seed biochemistry	HLH/MYC	Altered seed oil and protein content	988	(183-244)
989	G2417	Seed oil content	Seed biochemistry	GARP	Altered seed oil content	990	(235-285)
991	G2116	Seed oil content	Seed biochemistry	bZIP	Altered seed oil content	992	(150-210)
993	G647	Seed oil content	Seed biochemistry	Z-C3H	Altered seed oil content	994	(77-192)
995	G974	Seed oil and protein content	Seed biochemistry	AP2	Altered seed oil and protein content	996	(81-140)
997	G1419	Seed protein content	Seed biochemistry	AP2	Increased seed protein	998	(69-137)

Table 4

999	G1634	Seed protein content	Seed biochemistry	MYB-related	Altered seed protein content	1000	(129-180)
1001	G1637	Seed protein content	Seed biochemistry	MYB-related	Altered seed protein content	1002	(109-173)
1003	G1818	Seed protein content; flowering time	Seed biochemistry; flowering time	CAAT	Increased protein content; late flowering	1004	(36-113)
1005	G1820	Seed oil and protein content	Seed biochemistry	CAAT	Altered seed oil, protein content	1006	(70-133)
1007	G1903	Seed oil and protein content	Seed biochemistry	Z-Dof	Altered seed oil and protein content	1008	(134-180)
1009	G371	Seed oil and protein content	Seed biochemistry	RING/C3HC4	Altered seed oil and protein content	1010	(21-74)
1011	G597	Seed protein content	Seed biochemistry	AT-hook	Altered seed protein content	1012	(97-104,137-144)
1013	G1009	Seed protein content	Seed biochemistry	AP2	Altered seed protein content	1014	(201-277, 303-371)
1015	G170	Seed protein content	Seed biochemistry	MADS	Altered seed protein content	1016	(2-57)
1017	G1768	Seed protein content	Seed biochemistry	SCR	Altered seed protein content	1018	(54-413)
1019	G185	Seed protein content	Seed biochemistry	WRKY	Altered seed protein content	1020	(113-172)
1021	G1931	Seed protein content	Seed biochemistry	WRKY	Altered seed protein content	1022	(114-170)
1023	G2543	Seed protein content	Seed biochemistry	HB	Altered seed protein content	1024	(31-91)
1025	G264	Seed protein content	Seed biochemistry	HS	Altered seed protein content	1026	(24-114)
1027	G32	Seed protein content	Seed biochemistry	AP2	Altered seed protein content	1028	(17-84)
1029	G436	Seed protein content	Seed biochemistry	HB	Altered seed protein content	1030	(22-85)
1031	G556	Seed protein content	Seed biochemistry	bZIP	Altered seed protein content	1032	(83-143)
1033	G1420	Seed protein content	Seed biochemistry	WRKY	Altered seed protein content	1034	(221-280)
1035	G1412	Seed protein content	Seed biochemistry	NAC	Altered seed protein content	1036	(17-159)

Table 4

1037	G738	Seed protein content	Seed biochemistry	Z-Dof	Altered seed protein content	1038	(351-393)
1039	G2426	Seed protein content	Seed biochemistry	MYB-(R1)R2R3	Altered seed protein content	1040	(14-114)
1041	G1524	Seed protein content	Seed biochemistry	RING/C3HC4	Altered seed protein content	1042	(49-110)
1043	G1243	Seed protein content	Seed biochemistry	SWI/SNF	Altered seed protein content	1044	(216-609)
1045	G631	Seed protein content	Seed biochemistry	bZIP	Altered seed protein content	1046	(TBD)
1047	G1909	Seed protein content	Seed biochemistry	Z-Dof	Altered seed protein content	1048	(23-51)
1049	G1663	Seed protein content	Seed biochemistry	PCF	Altered seed protein content	1050	(TBD)
1051	G1231	Seed protein content	Seed biochemistry	Z-C4HC3	Altered seed protein content	1052	(TBD)
1053	G227	Seed protein content	Seed biochemistry	MYB-(R1)R2R3	Altered seed protein content	1054	(13-112)
1055	G1842	Seed protein content	Seed biochemistry	MADS	Altered seed protein content	1056	(2-57)
1057	G1505	Seed protein content	Seed biochemistry	GATA/Zn	Altered seed protein content	1058	(TBD)
1059	G657	Seed protein content	Seed biochemistry	MYB-(R1)R2R3	Altered seed protein content	1060	(TBD)
1061	G1959	Seed protein content	Seed biochemistry	GARP	Altered seed protein content	1062	(46-97)
1063	G2180	Seed protein content	Seed biochemistry	NAC	Altered seed protein content	1064	(7-156)
1065	G1817	Seed protein content	Seed biochemistry	PMR	Altered seed protein content	1066	(47-331)
1067	G1649	Seed protein content	Seed biochemistry	HLH/MYC	Altered seed protein content	1068	(225-295)
1069	G2131	Seed protein content	Seed biochemistry	AP2	Altered seed protein content	1070	(50-186, 112-183)
1071	G215	Seed protein content	Seed biochemistry	MYB-related	Altered seed protein content	1072	(TBD)
1073	G1508	Seed protein content	Seed biochemistry	GATA/Zn	Altered seed protein content	1074	(38-63)
1075	G2110	Seed protein content	Seed biochemistry	WRKY	Altered seed protein content	1076	(239-298)

Table 4

1077	G2442	Seed protein content	Seed biochemistry	RING/C3HC4	Altered seed protein content	1078	(220-246)
1079	G1051	Flowering time	Flowering time	bZIP	Late flowering	1080	(189-250)
1081	G1052	Flowering time	Flowering time	bZIP	Late flowering	1082	(201-261)
1083	G1079	Flowering time;	Flowering time;	BZIPT2	Late flowering; altered seed protein content	1084	(1-50)
1085	G1335	Flowering time	Flowering time	Z-CLDSH	Late flowering, slow growth	1086	(24-43, 131-144, 185-203)
1087	G157	Flowering time	Flowering time	MADS	Altered flowering; significant overexpression delays flowering time	1088	(2-57)
1089	G1895	Flowering time	Flowering time	Z-Dof	Late flowering	1090	(55-110)
1091	G1900	Flowering time	Flowering time	Z-Dof	Late flowering	1092	(54-106)
1093	G2007	Flowering time; seed protein content	Flowering time; seed biochemistry	MYB-(R1)R2R3	Late flowering; altered seed protein content	1094	(TBD)
1095	G214	Flowering time	Flowering time	MYB-related	Late flowering	1096	(22-71)
1097	G2155	Flowering time	Flowering time	AT-hook	Late flowering	1098	(18-38)
1099	G234	Flowering time	Flowering time	MYB-(R1)R2R3	Late flowering, small plant	1100	(14-115)
1101	G361	Flowering time	Flowering time	Z-C2H2	Late flowering	1102	(43-63)
1103	G562	Flowering time	Flowering time	bZIP	Late flowering	1104	(253-315)
1105	G591	Flowering time	Flowering time	HLH/MYC	Late flowering	1106	(143-240)
1107	G8	Flowering time	Flowering time	AP2	Late flowering	1108	(151-217, 243-296)
1109	G859	Flowering time; seed protein content	Flowering time; seed biochemistry	MADS	Late flowering; altered seed protein content	1110	(TBD)
1111	G878	Flowering time	Flowering time	WRKY	Late flowering	1112	(250-305, 415-475)
1113	G971	Flowering time	Flowering time	AP2	Late flowering	1114	(120-186)
1115	G975	Flowering time; morphology: other	Flowering time; dev and morph	AP2	Late flowering; glossy leaves	1116	(4-71)
1117	G994	Flowering time	Flowering time	MYB-(R1)R2R3	Late flowering, small	1118	(14-123)
1119	G2347	Flowering time	Flowering time	SBP	Late flowering, small	1120	(60-136)
1121	G2010	Flowering time	Flowering time	SBP	Late flowering	1122	(53-127)

Table 5

SEQ ID NO.	GID	Test Sequence ID	Smallest Sum Probability	Test Sequence Species	Test Sequence GenBank Annotation
859	G192	AW596933	7.70E-40	[Glycine max]	sj84f07.y1 Gm-c1034 Glycine max cDNA clone GENO
859	G192	AV423663	2.40E-39	[Lotus japonicus]	AV423663 Lotus japonicus young plants (two-
859	G192	BI422074	4.50E-34	[Lycopersicon esculentum]	EST532740 tomato callus, TAMU Lycop
859	G192	AW447931	1.40E-27	[Triticum aestivum]	BRY_1082 BRY Triticum aestivum cDNA clone
859	G192	BE998060	2.60E-24	[Medicago truncatula]	EST429783 GVSN Medicago truncatula cDNA
859	G192	AC018727	1.70E-23	[Oryza sativa]	chromosome 10 clone OSJNBa0056G17, *** SEQUENC
859	G192	BG600477	1.00E-20	[Solanum tuberosum]	EST505372 cSTS Solanum tuberosum cDNA clo
859	G192	BG356878	2.80E-16	[Sorghum bicolor]	OV2_11_B04.g1_A002 Ovary 2 (OV2) Sorghum bi
859	G192	gi12039364	1.10E-31	[Oryza sativa]	putative DNA-binding protein.
859	G192	gi4894963	3.30E-14	[Avena sativa]	DNA-binding protein WRKY3.
859	G192	gi1432056	5.80E-14	[Petroselinum crispum]	WRKY3.
859	G192	gi4760596	2.60E-13	[Nicotiana tabacum]	DNA-binding protein NtWRKY3.
859	G192	gi11993901	1.40E-12	[Dactylis glomerata]	somatic embryogenesis related protein.
859	G192	gi927025	7.60E-09	[Cucumis sativus]	SPF1-like DNA-binding protein.
859	G192	gi13620227	8.40E-09	[Lycopersicon esculentum]	hypothetical protein.
859	G192	gi3420906	2.80E-08	[Pimpinella brachycarpa]	zinc finger protein; WRKY1.
859	G192	gi1159877	4.70E-08	[Avena fatua]	DNA-binding protein.
859	G192	gi484261	1.60E-07	[Ipomoea batatas]	SPF1 protein.
801	G1946	LPHSF8	1.10E-119	[Lycopersicon peruvianum]	L.peruvianum Lp-hsf8 mRNA for heat
801	G1946	AC087771	4.10E-112	[Medicago truncatula]	clone 8D15, *** SEQUENCING IN PROGRESS
801	G1946	LEHSF8	5.90E-103	[Lycopersicon esculentum]	L.esculentum Le-hsf8 gene for heat
801	G1946	AW569138	3.10E-75	[Glycine max]	si63g09.y1 Gm-r1030 Glycine max cDNA clone GENO
801	G1946	BG890899	1.30E-70	[Solanum tuberosum]	EST516750 cSTD Solanum tuberosum cDNA clo
801	G1946	AC027658	4.60E-53	[Oryza sativa]	subsp. japonica BAC nbxb0006I13, chromosome 10
801	G1946	AV833112	4.90E-52	[Hordeum vulgare subsp. vulgare]	AV833112 K. Sato unpublished
801	G1946	gi19492	2.80E-121	[Lycopersicon peruvianum]	heat shock transcription factor 8
801	G1946	gi19260	5.10E-106	[Lycopersicon esculentum]	heat stress transcription factor
801	G1946	gi662924	2.00E-47	[Glycine max]	heat shock transcription factor 21.
801	G1946	gi5821138	9.70E-46	[Nicotiana tabacum]	heat shock factor.
801	G1946	gi11761077	2.90E-40	[Oryza sativa]	putative heat shock factor protein 1 (HSF 1)
801	G1946	gi886742	3.20E-40	[Zea mays]	heat shock factor.
801	G1946	gi7158882	2.70E-38	[Medicago sativa]	heat shock transcription factor.
801	G1946	gi3550588	1.90E-30	[Pisum sativum]	heat shock transcription factor (HSFA).

Table 5

801	G1946	gi100546	0.46	[Avena sativa]	avenin precursor - oat.
801	G1946	gi14190783	1	[Apium graveolens]	putative phloem transcription factor M1.
239	G375	AW696439	3.40E-33	[Medicago truncatula]	NF106B07ST1F1060 Developing stem Medica
239	G375	BG595870	1.90E-31	[Solanum tuberosum]	EST494548 cSTS Solanum tuberosum cDNA clo
239	G375	AI899263	3.70E-31	[Lycopersicon esculentum]	EST268706 tomato ovary, TAMU Lycope
239	G375	NTBBF3	4.00E-31	[Nicotiana tabacum]	N.tabacum mRNA for zinc finger protein, B
239	G375	BG405482	2.70E-30	[Glycine max]	sac44a11.y1 Gm-c1062 Glycine max cDNA clone GEN
239	G375	AB028130	3.30E-30	[Oryza sativa]	mRNA for Dof zinc finger protein, complete cds
239	G375	AB026297	7.30E-28	[Pisum sativum]	mRNA for elicitor-responsive Dof protein ERDP
239	G375	HVBPBF	1.10E-27	[Hordeum vulgare]	mRNA for DNA binding protein BPBF.
239	G375	BG263089	1.70E-27	[Triticum aestivum]	WHE2337_A02_A03ZS Wheat pre-anthesis spik
239	G375	ZMU82230	4.20E-27	[Zea mays]	endosperm-specific prolamin box binding factor (PB
239	G375	gi4996640	1.90E-37	[Oryza sativa]	Dof zinc finger protein.
239	G375	gi3777436	8.10E-35	[Hordeum vulgare]	DNA binding protein.
239	G375	gi2393775	1.10E-33	[Zea mays]	prolamin box binding factor.
239	G375	gi1360088	2.00E-33	[Nicotiana tabacum]	Zn finger protein.
239	G375	gi3790264	4.30E-32	[Triticum aestivum]	PBF protein.
239	G375	gi6092016	1.30E-29	[Pisum sativum]	elicitor-responsive Dof protein ERDP.
239	G375	gi7688355	5.60E-29	[Solanum tuberosum]	Dof zinc finger protein.
239	G375	gi1669341	4.60E-20	[Cucurbita maxima]	AOBP (ascorbate oxidase promoter-binding
239	G375	gi3929325	5.50E-18	[Dendrobium grex Madame Thong-In]	putative DNA-binding prot
239	G375	gi19547	5.50E-06	[Medicago sativa subsp. falcata]	environmental stress and a
273	G1255	AC087181	1.60E-46	[Oryza sativa]	chromosome 3 clone OSJNBa0018H01, *** SEQUENCI
273	G1255	BG239774	4.50E-33	[Glycine max]	sab74c03.y1 Gm-c1032 Glycine max cDNA clone GEN
273	G1255	BG321336	1.70E-32	[Descurainia sophia]	Ds01_06h10_A Ds01_AAFC_ECORC_cold_stress
273	G1255	AI772841	2.90E-30	[Lycopersicon esculentum]	EST253941 tomato resistant, Cornell
273	G1255	BF480245	4.60E-29	[Mesembryanthemum crystallinum]	L0-2152T3 Ice plant Lambda Un
273	G1255	AW688119	2.10E-28	[Medicago truncatula]	NF002E07ST1F1000 Developing stem Medica
273	G1255	BF266327	1.80E-26	[Hordeum vulgare]	HV_CEa0014N02f Hordeum vulgare seedling gre
273	G1255	AW671538	5.80E-25	[Sorghum bicolor]	LG1_348_B08.b1_A002 Light Grown 1 (LG1) Sor
273	G1255	BI072021	5.30E-20	[Populus tremula x Populus tremuloides]	C067P76U Populus stra
273	G1255	BG273908	4.90E-19	[Vitis vinifera]	EST 110 Green Grape berries Lambda Zap II Li
273	G1255	gi13702811	3.70E-52	[Oryza sativa]	putative zinc finger protein.
273	G1255	gi11037311	4.00E-21	[Brassica nigra]	constans-like protein.
273	G1255	gi2303683	1.10E-19	[Brassica napus]	unnamed protein product.
273	G1255	gi4091804	2.30E-18	[Malus x domestica]	CONSTANS-like protein 1.

Table 5

273	G1255	gi3341723	4.30E-18	[Raphanus sativus]	CONSTANS-like 1 protein.
273	G1255	gi10946337	5.20E-17	[Ipomoea nil]	CONSTANS-like protein.
273	G1255	gi4557093	3.30E-15	[Pinus radiata]	zinc finger protein.
273	G1255	gi8132543	0.97	[Chloroplast Zamia furfuracea]	cytochrome b559 alpha subuni
273	G1255	gi11795	0.99	[Nicotiana tabacum]	put. psbE protein (aa 1-83).
273	G1255	gi65646	0.99	[Chloroplast Nicotiana tabacum]	cytochrome b559 component p
557	G865	BE419451	3.70E-32	[Triticum aestivum]	WWS012.C2R000101 ITEC WWS Wheat Scutellum
557	G865	AW560968	1.10E-28	[Medicago truncatula]	EST316016 DSIR Medicago truncatula cDNA
557	G865	AW782252	1.20E-26	[Glycine max]	sm03d11.y1 Gm-c1027 Glycine max cDNA clone GENO
557	G865	BI421895	3.60E-25	[Lycopersicon esculentum]	EST532561 tomato callus, TAMU Lycop
557	G865	BE642320	1.60E-24	[Ceratopteris richardii]	Cri2_5_L17_SP6 Ceratopteris Spore Li
557	G865	BE494041	1.60E-24	[Secale cereale]	WHE1277_B09_D17ZS Secale cereale anther cDNA
557	G865	D39914	2.60E-24	[Oryza sativa]	RICS1576A Rice shoot Oryza sativa cDNA, mRNA s
557	G865	AV428124	9.00E-23	[Lotus japonicus]	AV428124 Lotus japonicus young plants (two-
557	G865	TOBBY4D	1.80E-21	[Nicotiana tabacum]	Tobacco mRNA for EREBP-2, complete cds.
557	G865	gi1208495	2.40E-23	[Nicotiana tabacum]	ERF1.
557	G865	gi8809571	5.10E-23	[Nicotiana sylvestris]	ethylene-responsive element binding
557	G865	gi3342211	1.40E-22	[Lycopersicon esculentum]	Pti4.
557	G865	gi7528276	1.70E-22	[Mesembryanthemum crystallinum]	AP2-related transcription f
557	G865	gi15217291	7.80E-22	[Oryza sativa]	Putative AP2 domain containing protein.
557	G865	gi3264767	2.70E-21	[Prunus armeniaca]	AP2 domain containing protein.
557	G865	gi8980313	2.10E-20	[Catharanthus roseus]	AP2-domain DNA-binding protein.
557	G865	gi8571476	9.30E-20	[Atriplex hortensis]	apetala2 domain-containing protein.
557	G865	gi1688233	1.40E-19	[Solanum tuberosum]	DNA binding protein homolog.
557	G865	gi6478845	1.80E-19	[Matricaria chamomilla]	ethylene-responsive element binding
23	G2509	BH577856	2.50E-29	[Brassica oleracea]	BOHOJ67TR BOHO Brassica oleracea genomic
23	G2509	BM269574	5.90E-28	[Glycine max]	sak01e08.y1 Gm-c1074 Glycine max cDNA clone SOY
23	G2509	BE419451	2.20E-27	[Triticum aestivum]	WWS012.C2R000101 ITEC WWS Wheat Scutellum
23	G2509	AI483636	7.80E-27	[Lycopersicon esculentum]	EST249507 tomato ovary, TAMU Lycope
23	G2509	AW560968	8.90E-27	[Medicago truncatula]	EST316016 DSIR Medicago truncatula cDNA
23	G2509	BE642320	4.30E-26	[Ceratopteris richardii]	Cri2_5_L17_SP6 Ceratopteris Spore Li
23	G2509	AP003286	1.00E-25	[Oryza sativa]	chromosome 1 clone P0677H08, *** SEQUENCING IN
23	G2509	BE494041	3.20E-25	[Secale cereale]	WHE1277_B09_D17ZS Secale cereale anther cDNA
23	G2509	BE602106	1.10E-24	[Hordeum vulgare]	HVSMEh0102I06f Hordeum vulgare 5-45 DAP spi
23	G2509	AV428124	1.00E-23	[Lotus japonicus]	AV428124 Lotus japonicus young plants (two-
23	G2509	gi3264767	4.00E-27	[Prunus armeniaca]	AP2 domain containing protein.

Table 5

23	G2509	gi12003376	1.40E-23	[Nicotiana tabacum]	Avr9/Cf-9 rapidly elicited protein 1.
23	G2509	gi14140141	2.30E-23	[Oryza sativa]	putative AP2-related transcription factor.
23	G2509	gi1688233	5.40E-23	[Solanum tuberosum]	DNA binding protein homolog.
23	G2509	gi4099921	2.60E-22	[Stylosanthes hamata]	EREBP-3 homolog.
23	G2509	gi8809571	7.80E-22	[Nicotiana sylvestris]	ethylene-responsive element binding
23	G2509	gi3342211	1.00E-21	[Lycopersicon esculentum]	Pti4.
23	G2509	gi7528276	2.70E-21	[Mesembryanthemum crystallinum]	AP2-related transcription f
23	G2509	gi17385636	1.90E-20	[Matricaria chamomilla]	ethylene-responsive element binding
23	G2509	gi18496063	3.30E-20	[Fagus sylvatica]	ethylene responsive element binding prote
1119	G2347	BI931517	5.30E-31	[Lycopersicon esculentum]	EST551406 tomato flower, 8 mm to pr
1119	G2347	BE058432	4.20E-29	[Glycine max]	sn16a06.y1 Gm-c1016 Glycine max cDNA clone GENO
1119	G2347	AMSPB1	1.80E-28	[Antirrhinum majus]	A.majus mRNA for squamosa-promoter bindin
1119	G2347	BG525285	5.70E-28	[Stevia rebaudiana]	48-3 Stevia field grown leaf cDNA Stevia
1119	G2347	L38193	4.60E-27	[Brassica rapa]	BNAF1025E Mustard flower buds Brassica rapa c
1119	G2347	BG455868	6.40E-27	[Medicago truncatula]	NF068F05PL1F1045 Phosphate starved leaf
1119	G2347	BG097153	1.70E-24	[Solanum tuberosum]	EST461672 potato leaves and petioles Sola
1119	G2347	BF482644	1.60E-23	[Triticum aestivum]	WHE2301-2304_A21_A21ZS Wheat pre-anthesis
1119	G2347	AW747167	2.30E-23	[Sorghum bicolor]	WS1_66_F11.b1_A002 Water-stressed 1 (WS1) S
1119	G2347	BG442540	2.50E-23	[Gossypium arboreum]	GA__Ea0017G06f Gossypium arboreum 7-10 d
1119	G2347	gi1183864	1.50E-31	[Antirrhinum majus]	squamosa-promoter binding protein 2.
1119	G2347	gi5931786	3.40E-25	[Zea mays]	SBP-domain protein 5.
1119	G2347	gi8468036	1.40E-21	[Oryza sativa]	Similar to Arabidopsis thaliana chromosome 2
1119	G2347	gi9087308	6.60E-09	[Mitochondrion Beta vulgaris var. altissima]	orf102a.
1119	G2347	gi7209500	0.83	[Brassica rapa]	S-locus pollen protein.
43	G988	CRU303349	3.10E-208	[Capsella rubella]	ORF1, ORF2, ORF3, ORF4, ORF5 and ORF6 (pa
43	G988	A84072	4.50E-86	[Lycopersicon esculentum]	Sequence 1 from Patent WO9846759.
43	G988	A84080	3.30E-85	[Solanum tuberosum]	Sequence 9 from Patent WO9846759.
43	G988	AP003944	1.30E-57	[Oryza sativa]	chromosome 6 clone OJ1126_F05, *** SEQUENCING
43	G988	AX081276	2.80E-43	[Brassica napus]	Sequence 1 from Patent WO0109356.
43	G988	ZMA242530	1.50E-40	[Zea mays]	partial d8 gene for gibberellin response modulato
43	G988	AX005804	2.50E-37	[Triticum aestivum]	Sequence 13 from Patent WO9909174.
43	G988	AB048713	9.10E-33	[Pisum sativum]	PsSCR mRNA for SCARECROW, complete cds.
43	G988	AW774515	2.00E-29	[Medicago truncatula]	EST333666 KV3 Medicago truncatula cDNA
43	G988	BE822458	1.20E-27	[Glycine max]	GM700017A20H12 Gm-r1070 Glycine max cDNA clone
43	G988	gi13620166	8.00E-211	[Capsella rubella]	hypothetical protein.
43	G988	gi4160441	1.40E-87	[Lycopersicon esculentum]	lateral suppressor protein.

Table 5

43	G988	gi10178637	2.20E-48	[Zea mays]	SCARECROW.
43	G988	gi6970472	1.20E-47	[Oryza sativa]	OsGAI.
43	G988	gi5640157	2.80E-45	[Triticum aestivum]	gibberellin response modulator.
43	G988	gi13170126	7.10E-45	[Brassica napus]	unnamed protein product.
43	G988	gi13365610	1.10E-40	[Pisum sativum]	SCARECROW.
43	G988	gi14318115	1.10E-14	[Zea mays subsp. mays]	gibberellin response modulator.
43	G988	gi14318165	7.30E-14	[Tripsacum dactyloides]	gibberellin response modulator.
43	G988	gi347457	2.40E-05	[Glycine max]	hydroxyproline-rich glycoprotein.
459	G2346	AMA011622	3.10E-35	[Antirrhinum majus]	mRNA for squamosa promoter binding
459	G2346	AW691786	1.80E-26	[Medicago truncatula]	NF044B06ST1F1000 Developing stem Medica
459	G2346	AQ273505	7.00E-25	[Oryza sativa]	nbxb0030O03f CUGI Rice BAC Library Oryza sativ
459	G2346	AW932595	7.90E-24	[Lycopersicon esculentum]	EST358438 tomato fruit mature green
459	G2346	BG593787	9.50E-24	[Solanum tuberosum]	EST492465 cSTS Solanum tuberosum cDNA clo
459	G2346	BG442540	1.00E-23	[Gossypium arboreum]	GA__Ea0017G06f Gossypium arboreum 7-10 d
459	G2346	AZ919034	1.90E-23	[Zea mays]	1006013G02.x3 1006 - RescueMu Grid G Zea mays geno
459	G2346	BE596165	2.70E-23	[Sorghum bicolor]	PI1_50_D04.b1_A002 Pathogen induced 1 (PI1)
459	G2346	AI443033	2.30E-22	[Glycine max]	sa31a08.y1 Gm-c1004 Glycine max cDNA clone GENO
459	G2346	BF482644	4.30E-22	[Triticum aestivum]	WHE2301-2304_A21_A21ZS Wheat pre-anthesis
459	G2346	gi5931643	6.20E-45	[Antirrhinum majus]	squamosa promoter binding protein-homol
459	G2346	gi5931786	4.20E-26	[Zea mays]	SBP-domain protein 5.
459	G2346	gi8468036	3.30E-14	[Oryza sativa]	Similar to Arabidopsis thaliana chromosome 2
459	G2346	gi9087308	8.30E-08	[Mitochondrion Beta vulgaris var. altissima]	orf102a.
285	G1354	BG128374	2.90E-58	[Lycopersicon esculentum]	EST474020 tomato shoot/meristem Lyc
285	G1354	BE202831	1.90E-56	[Medicago truncatula]	EST402853 KV1 Medicago truncatula cDNA
285	G1354	AI161918	6.60E-55	[Populus tremula x Populus tremuloides]	A009P50U Hybrid aspen
285	G1354	AB028186	1.20E-53	[Oryza sativa]	mRNA for OsNAC7 protein, complete cds.
285	G1354	BE060921	8.00E-50	[Hordeum vulgare]	HVSMEg0013N15f Hordeum vulgare pre-anthesis
285	G1354	AF402603	1.50E-42	[Phaseolus vulgaris]	NAC domain protein NAC2 mRNA, complete c
285	G1354	BE357920	1.60E-42	[Sorghum bicolor]	DG1_23_F03.b1_A002 Dark Grown 1 (DG1) Sorgh
285	G1354	PHRNANAM	3.60E-42	[Petunia x hybrida]	P.hybrida mRNA encoding NAM protein.
285	G1354	AW185617	5.30E-40	[Glycine max]	se80b05.y1 Gm-c1023 Glycine max cDNA clone GENO
285	G1354	gi6006373	4.50E-63	[Oryza sativa]	Similar to NAM like protein (AC005310).
285	G1354	gi15148914	2.30E-44	[Phaseolus vulgaris]	NAC domain protein NAC2.
285	G1354	gi14485513	3.50E-44	[Solanum tuberosum]	putative NAC domain protein.
285	G1354	gi1279640	5.90E-44	[Petunia x hybrida]	NAM.
285	G1354	gi6175246	5.20E-41	[Lycopersicon esculentum]	jasmonic acid 2.

Table 5

285	G1354	gi4218535	5.10E-39	[Triticum sp.]	GRAB1 protein.
285	G1354	gi6732158	5.10E-39	[Triticum monococcum]	unnamed protein product.
285	G1354	gi7716952	3.30E-35	[Medicago truncatula]	NAC1.
285	G1354	gi4996349	2.50E-26	[Nicotiana tabacum]	NAC-domain protein.
285	G1354	gi2982275	3.10E-14	[Picea mariana]	ATAF1-like protein.
119	G1063	BH700922	4.50E-90	[Brassica oleracea]	BOMMZ07TR BO_2_3_KB Brassica oleracea gen
119	G1063	BE451174	2.40E-41	[Lycopersicon esculentum]	EST402062 tomato root, plants pre-a
119	G1063	AW832545	2.00E-40	[Glycine max]	sm12e10.y1 Gm-c1027 Glycine max cDNA clone GENO
119	G1063	AP004693	5.90E-37	[Oryza sativa]	chromosome 8 clone P0461F06, *** SEQUENCING IN
119	G1063	AP004462	4.40E-32	[Oryza sativa (japonica cultivar-group)]	( ) chromosome 8 clo
119	G1063	AT002234	8.90E-32	[Brassica rapa subsp. pekinensis]	AT002234 Flower bud cDNA Br
119	G1063	BF263465	5.40E-25	[Hordeum vulgare]	HV_CEa0006N02f Hordeum vulgare seedling gre
119	G1063	BG557011	4.20E-22	[Sorghum bicolor]	EM1_41_E02.g1_A002 Embryo 1 (EM1) Sorghum b
119	G1063	BG842856	3.10E-21	[Zea mays]	MEST40-H05.T3 ISUM4-TN Zea mays cDNA clone MEST40-
119	G1063	BG559930	1.40E-18	[Sorghum propinquum]	RHIZ2_75_D09.g1_A003 Rhizome2 (RHIZ2) So
119	G1063	gi15528743	4.20E-26	[Oryza sativa]	contains EST C74560(E31855)~unknown protein.
119	G1063	gi6166283	8.10E-10	[Pinus taeda]	helix-loop-helix protein 1A.
119	G1063	gi11045087	8.80E-09	[Brassica napus]	putative protein.
119	G1063	gi10998404	7.10E-08	[Petunia x hybrida]	anthocyanin 1.
119	G1063	gi99441	2.60E-07	[Volvox carteri]	sulfated surface glycoprotein 185 - Volvox
119	G1063	gi1142621	5.00E-07	[Phaseolus vulgaris]	phaseolin G-box binding protein PG2.
119	G1063	gi166428	8.10E-07	[Antirrhinum majus]	DEL.
119	G1063	gi1247386	9.50E-07	[Nicotiana alata]	PRP2.
119	G1063	gi82091	1.00E-06	[Lycopersicon esculentum]	hydroxyproline-rich glycoprotein
119	G1063	gi1486263	1.40E-06	[Catharanthus roseus]	extensin.
129	G2143	BH650724	3.00E-88	[Brassica oleracea]	BOMIW43TR BO_2_3_KB Brassica oleracea gen
129	G2143	AW832545	1.50E-40	[Glycine max]	sm12e10.y1 Gm-c1027 Glycine max cDNA clone GENO
129	G2143	BE451174	3.50E-40	[Lycopersicon esculentum]	EST402062 tomato root, plants pre-a
129	G2143	AP004693	4.00E-38	[Oryza sativa]	chromosome 8 clone P0461F06, *** SEQUENCING IN
129	G2143	AP004584	6.30E-33	[Oryza sativa (japonica cultivar-group)]	( ) chromosome 8 clo
129	G2143	AT002234	3.00E-31	[Brassica rapa subsp. pekinensis]	AT002234 Flower bud cDNA Br
129	G2143	BF263465	2.90E-26	[Hordeum vulgare]	HV_CEa0006N02f Hordeum vulgare seedling gre
129	G2143	BG557011	2.60E-22	[Sorghum bicolor]	EM1_41_E02.g1_A002 Embryo 1 (EM1) Sorghum b
129	G2143	BG842856	3.50E-20	[Zea mays]	MEST40-H05.T3 ISUM4-TN Zea mays cDNA clone MEST40-
129	G2143	BG559930	6.10E-18	[Sorghum propinquum]	RHIZ2_75_D09.g1_A003 Rhizome2 (RHIZ2) So
129	G2143	gi15528743	5.50E-26	[Oryza sativa]	contains EST C74560(E31855)~unknown protein.

Table 5

129	G2143	gi1086538	7.60E-09	[Oryza rufipogon]	transcriptional activator Rb homolog.
129	G2143	gi6166283	1.10E-08	[Pinus taeda]	helix-loop-helix protein 1A.
129	G2143	gi1142621	4.60E-07	[Phaseolus vulgaris]	phaseolin G-box binding protein PG2.
129	G2143	gi3399777	5.20E-07	[Glycine max]	symbiotic ammonium transporter; nodulin.
129	G2143	gi5923912	6.10E-07	[Tulipa gesneriana]	bHLH transcription factor GBOF-1.
129	G2143	gi10998404	9.20E-07	[Petunia x hybrida]	anthocyanin 1.
129	G2143	gi4321762	5.20E-06	[Zea mays]	transcription factor MYC7E.
129	G2143	gi166428	6.00E-06	[Antirrhinum majus]	DEL.
129	G2143	gi527665	7.40E-06	[Sorghum bicolor]	myc-like regulatory R gene product.
133	G2557	BH511840	6.70E-62	[Brassica oleracea]	BOGRJ19TR BOGR Brassica oleracea genomic
133	G2557	BE347811	3.70E-46	[Glycine max]	sp05h10.y1 Gm-c1041 Glycine max cDNA clone GENO
133	G2557	AP003141	2.40E-33	[Oryza sativa]	genomic DNA, chromosome 1, PAC clone:P0002B05,
133	G2557	BF263465	3.00E-31	[Hordeum vulgare]	HV_CEa0006N02f Hordeum vulgare seedling gre
133	G2557	AT002234	6.60E-27	[Brassica rapa subsp. pekinensis]	AT002234 Flower bud cDNA Br
133	G2557	BG557011	6.40E-26	[Sorghum bicolor]	EM1_41_E02.g1_A002 Embryo 1 (EM1) Sorghum b
133	G2557	AP004462	7.90E-26	[Oryza sativa (japonica cultivar-group)]	( ) chromosome 8 clo
133	G2557	BE451174	3.90E-25	[Lycopersicon esculentum]	EST402062 tomato root, plants pre-a
133	G2557	BG842856	5.60E-22	[Zea mays]	MEST40-H05.T3 ISUM4-TN Zea mays cDNA clone MEST40-
133	G2557	BG559930	7.00E-14	[Sorghum propinquum]	RHIZ2_75_D09.g1_A003 Rhizome2 (RHIZ2) So
133	G2557	gi15289790	2.40E-36	[Oryza sativa]	contains EST C74560(E31855)~unknown protein.
133	G2557	gi3399777	2.60E-06	[Glycine max]	symbiotic ammonium transporter; nodulin.
133	G2557	gi4206118	1.10E-05	[Mesembryanthemum crystallinum]	transporter homolog.
133	G2557	gi6166283	1.30E-05	[Pinus taeda]	helix-loop-helix protein 1A.
133	G2557	gi527655	3.70E-05	[Pennisetum glaucum]	myc-like regulatory R gene product.
133	G2557	gi5923912	3.70E-05	[Tulipa gesneriana]	bHLH transcription factor GBOF-1.
133	G2557	gi527661	7.80E-05	[Phyllostachys acuta]	myc-like regulatory R gene product.
133	G2557	gi527665	9.50E-05	[Sorghum bicolor]	myc-like regulatory R gene product.
133	G2557	gi1086538	0.0001	[Oryza rufipogon]	transcriptional activator Rb homolog.
133	G2557	gi5669656	0.00013	[Lycopersicon esculentum]	ER33 protein.
697	G2430	BF632520	1.90E-14	[Medicago truncatula]	NF039A08DT1F1054 Drought Medicago trunc
697	G2430	AW396912	1.20E-13	[Glycine max]	sg64g09.y1 Gm-c1007 Glycine max cDNA clone GENO
697	G2430	D41804	4.50E-13	[Oryza sativa]	RICS4626A Rice shoot Oryza sativa cDNA, mRNA s
697	G2430	BE214029	2.60E-10	[Hordeum vulgare]	HV_CEb0001P06f Hordeum vulgare seedling gre
697	G2430	AW564570	2.70E-10	[Sorghum bicolor]	LG1_296_E01.b1_A002 Light Grown 1 (LG1) Sor
697	G2430	BG129795	5.40E-10	[Lycopersicon esculentum]	EST475441 tomato shoot/meristem Lyc
697	G2430	AB060130	5.40E-09	[Zea mays]	ZmRR8 mRNA for response regulator 8, complete cds.

Table 5

697	G2430	BF587105	2.50E-05	[Sorghum propinquum]	FM1_32_C05.b1_A003 Floral-Induced Merist
697	G2430	AI163121	0.3	[Populus tremula x Populus tremuloides]	A033P70U Hybrid aspen
697	G2430	BG595628	0.46	[Solanum tuberosum]	EST494306 cSTS Solanum tuberosum cDNA clo
697	G2430	gi13661174	5.40E-18	[Zea mays]	response regulator 8.
697	G2430	gi15289981	0.028	[Oryza sativa]	hypothetical protein.
697	G2430	gi6942190	0.12	[Mesembryanthemum crystallinum]	CDPK substrate protein 1; C
697	G2430	gi4519671	0.2	[Nicotiana tabacum]	transfactor.
831	G1478	BF275913	1.50E-20	[Gossypium arboreum]	GA__Eb0025C07f Gossypium arboreum 7-10 d
831	G1478	BG157399	6.50E-19	[Glycine max]	sab36g12.y1 Gm-c1026 Glycine max cDNA clone GEN
831	G1478	C95300	2.20E-10	[Citrus unshiu]	C95300 Citrus unshiu Miyagawa-wase maturation
831	G1478	AW034552	2.70E-10	[Lycopersicon esculentum]	EST278168 tomato callus, TAMU Lycop
831	G1478	BI070429	3.40E-10	[Populus tremula x Populus tremuloides]	C037P68U Populus stra
831	G1478	AF016011	5.10E-09	[Brassica napus]	CONSTANS homolog (Bn9CON10) gene, complete c
831	G1478	BE598912	6.20E-09	[Sorghum bicolor]	PI1_84_H11.b1_A002 Pathogen induced 1 (PI1)
831	G1478	BG605313	6.80E-09	[Triticum aestivum]	WHE2331_C04_F07ZS Wheat pre-anthesis spik
831	G1478	BE558327	8.90E-09	[Hordeum vulgare]	HV_CEb0017D19f Hordeum vulgare seedling gre
831	G1478	BG647091	1.20E-08	[Medicago truncatula]	EST508710 HOGA Medicago truncatula cDNA
831	G1478	gi2895188	4.70E-11	[Brassica napus]	CONSTANS homolog.
831	G1478	gi3618308	1.50E-09	[Oryza sativa]	zinc finger protein.
831	G1478	gi11037308	4.70E-09	[Brassica nigra]	constans-like protein.
831	G1478	gi3341723	1.30E-08	[Raphanus sativus]	CONSTANS-like 1 protein.
831	G1478	gi4091806	1.50E-07	[Malus x domestica]	CONSTANS-like protein 2.
831	G1478	gi10946337	3.10E-07	[Ipomoea nil]	CONSTANS-like protein.
831	G1478	gi4557093	1.40E-05	[Pinus radiata]	zinc finger protein.
831	G1478	gi619312	0.9	[Capparis masaikai]	mabinlin III B-chain=sweet protein mabi
831	G1478	gi4732091	1	[Zea mays]	bundle sheath defective protein 2.
831	G1478	gi4699629	1	[Nicotiana alata]	Chain A, Putative Ancestral Protein Encod
579	G681	BG128147	6.80E-41	[Lycopersicon esculentum]	EST473793 tomato shoot/meristem Lyc
579	G681	BF054497	1.50E-39	[Solanum tuberosum]	EST439727 potato leaves and petioles Sola
579	G681	BE054276	8.40E-39	[Gossypium arboreum]	GA__Ea0002O18f Gossypium arboreum 7-10 d
579	G681	BG269414	4.00E-38	[Mesembryanthemum crystallinum]	L0-3478T3 Ice plant Lambda Un
579	G681	BF620286	7.40E-38	[Hordeum vulgare]	HVSMEc0019F08f Hordeum vulgare seedling sho
579	G681	BE490032	1.00E-37	[Triticum aestivum]	WHE0364_C04_E08ZS Wheat cold-stressed see
579	G681	BI542536	1.40E-36	[Zea mays]	949021A03.y1 949 - Juvenile leaf and shoot cDNA fr
579	G681	BF425254	7.20E-36	[Glycine max]	su42c10.y1 Gm-c1068 Glycine max cDNA clone GENO
579	G681	AW672062	3.20E-34	[Sorghum bicolor]	LG1_354_G05.b1_A002 Light Grown 1 (LG1) Sor

Table 5

579	G681	BG448527	1.00E-33	[Medicago truncatula]	NF036F04RT1F1032 Developing root Medica
579	G681	gi13346188	9.10E-37	[Gossypium hirsutum]	GHMYB25.
579	G681	gi20563	6.30E-36	[Petunia x hybrida]	protein 1.
579	G681	gi485867	1.20E-34	[Antirrhinum majus]	mixta.
579	G681	gi2605617	1.70E-32	[Oryza sativa]	OSMYB1.
579	G681	gi1430846	2.00E-31	[Lycopersicon esculentum]	myb-related transcription factor.
579	G681	gi6651292	2.20E-30	[Pimpinella brachycarpa]	myb-related transcription factor.
579	G681	gi15042116	4.90E-30	[Zea mays subsp. parviglumis]	CI protein.
579	G681	gi82730	6.10E-30	[Zea mays]	transforming protein (myb) homolog (clone Zm38)
579	G681	gi5139806	8.30E-30	[Glycine max]	GmMYB29A2.
579	G681	gi19055	1.10E-29	[Hordeum vulgare]	MybHv5.
611	G878	AF096299	6.20E-90	[Nicotiana tabacum]	DNA-binding protein 2 (WRKY2) mRNA, compl
611	G878	CUSSLDB	1.80E-83	[Cucumis sativus]	SPF1-like DNA-binding protein mRNA, complet
611	G878	AF193802	3.50E-63	[Oryza sativa]	zinc finger transcription factor WRKY1 mRNA, c
611	G878	AX192162	2.20E-62	[Glycine max]	Sequence 9 from Patent WO0149840.
611	G878	IPBSPF1P	3.80E-58	[Ipomoea batatas]	Sweet potato mRNA for SPF1 protein, complet
611	G878	AFABF1	2.00E-56	[Avena fatua]	A.fatua mRNA for DNA-binding protein (clone ABF
611	G878	LES303343	7.20E-55	[Lycopersicon esculentum]	mRNA for hypothetical protein (ORF
611	G878	AX192164	4.00E-54	[Triticum aestivum]	Sequence 11 from Patent WO0149840.
611	G878	AF080595	2.10E-53	[Pimpinella brachycarpa]	zinc finger protein (ZFP1) mRNA, com
611	G878	PCU48831	2.30E-53	[Petroselinum crispum]	DNA-binding protein WRKY1 mRNA, comple
611	G878	gi4322940	3.30E-128	[Nicotiana tabacum]	DNA-binding protein 2.
611	G878	gi927025	1.10E-109	[Cucumis sativus]	SPF1-like DNA-binding protein.
611	G878	gi6689916	1.50E-74	[Oryza sativa]	zinc finger transcription factor WRKY1.
611	G878	gi484261	1.10E-66	[Ipomoea batatas]	SPF1 protein.
611	G878	gi1159877	2.30E-63	[Avena fatua]	DNA-binding protein.
611	G878	gi13620227	4.60E-63	[Lycopersicon esculentum]	hypothetical protein.
611	G878	gi5917653	1.70E-56	[Petroselinum crispum]	zinc-finger type transcription facto
611	G878	gi4894965	5.00E-56	[Avena sativa]	DNA-binding protein WRKY1.
611	G878	gi3420906	8.70E-56	[Pimpinella brachycarpa]	zinc finger protein; WRKY1.
611	G878	gi13620168	4.20E-22	[Capsella rubella]	hypothetical protein.
47	G374	AP004457	1.20E-73	[Oryza sativa (japonica cultivar-group)]	( ) chromosome 8 clo
47	G374	AP004693	1.90E-73	[Oryza sativa]	chromosome 8 clone P0461F06, *** SEQUENCING IN
47	G374	BH552835	1.30E-62	[Brassica oleracea]	BOHGT56TR BOHG Brassica oleracea genomic
47	G374	BG128229	6.50E-55	[Lycopersicon esculentum]	EST473875 tomato shoot/meristem Lyc
47	G374	BG646959	3.20E-46	[Medicago truncatula]	EST508578 HOGA Medicago truncatula cDNA

Table 5

47	G374	BG890162	8.70E-41	[Solanum tuberosum]	EST516013 cSTD Solanum tuberosum cDNA clo
47	G374	AW179366	6.00E-38	[Zea mays]	618046G06.y1 618 - Inbred Tassel cDNA Library Zea
47	G374	BF473206	1.50E-32	[Triticum aestivum]	WHE0922_G12_M24ZS Wheat 5-15 DAP spike cD
47	G374	AW761011	2.90E-29	[Glycine max]	sl61g11.y1 Gm-c1027 Glycine max cDNA clone GENO
47	G374	AJ436050	1.50E-27	[Hordeum vulgare]	AJ436050 S00007 Hordeum vulgare cDNA clone
47	G374	gi422012	0.8	[Sorghum bicolor]	lipid transfer protein - sorghum (fragmen
47	G374	gi1827893	1	[Zea mays]	Maize Nonspecific Lipid Transfer Protein Complex

Traits of interest

Examples of some of the traits that may be desirable in plants, and that may be provided by transforming the plants with the presently disclosed sequences, are listed in Table 6.

Table 6. Genes, traits and utilities that affect plant characteristics

Trait Category	Traits	Transcription factor genes that impact traits	Utility Gene effect on:
Resistance and tolerance	Salt stress resistance	G22; G196; G226; G303; G312; G325; G353; G482; G545; G801; G867; G884; G922; G926; G1452; G1794; G1820; G1836; G1843; G1863; G2053; G2110; G2140; G2153; G2379; G2701; G2713; G2719; G2789	Germination rate, survivability, yield; extended growth range
	Osmotic stress resistance	G47; G175; G188; G303; G325; G353; G489; G502; G526; G921; G922; G926; G1069; G1089; G1452; G1794; G1930; G2140; G2153; G2379; G2701; G2719; G2789;	Germination rate, survivability, yield
	Cold stress resistance; cold germination	G256; G394; G664;G864;G1322; G2130	Germination, growth, earlier planting
	Tolerance to freezing	G303; G325; G353; G720; G912; G913; G1794; G2053; G2140; G2153; G2379; G2701; G2719; G2789	Survivability, yield, appearance, extended range
	Heat stress resistance	G3; G464; G682; G864; G964;	Germination,

		G1305; G1645; G2130 G2430	growth, later planting
	Drought, low humidity resistance	G303; G325; G353; G720; G912; G926; G1452; G1794; G1820; G1843; G2053; G2140; G2153; G2379; G2583; G2701; G2719; G2789	Survivability, yield, extended range
	Radiation resistance	G1052	Survivability, vigor, appearance
	Decreased herbicide sensitivity	G343; G2133; G2517	Resistant to increased herbicide use
	Increased herbicide sensitivity	G374; G877;G1519	Use as a herbicide target
	Oxidative stress	G477; G789; G1807; G2133; G2517	Improved yield, appearance, reduced senescence
	Light response	G183; G354; G375; G1062; G1322; G1331; G1488; G1494; G1521; G1786; G1794; G2144; G2555;	Germination, growth, development, flowering time
Development, morphology	Overall plant architecture	G24; G27; G31; G33; G47; G147; G156; G160; G182; G187; G195; G196; G211; G221; G237; G280; G342; G352; G357; G358; G360; G362; G364; G365; G367; G373; G377; G396; G431; G447; G479; G546; G546; G551; G578; G580; G596; G615; G617; G620; G625;	Vascular tissues, lignin content; cell wall content; appearance

		G638; G658; G716; G725; G727; G730; G740; G770; G858; G865; G869; G872; G904; G910; G912; G920; G939; G963; G977; G979; G987; G988; G993; G1007; G1010; G1014; G1035; G1046; G1049; G1062; G1069; G1070; G1076; G1089; G1093; G1127; G1131; G1145; G1229; G1246; G1304; G1318; G1320; G1330; G1331; G1352; G1354; G1360; G1364; G1379; G1384; G1399; G1415; G1417; G1442; G1453; G1454; G1459; G1460; G1471; G1475; G1477; G1487; G1487; G1492; G1499; G1499; G1531; G1540; G1543; G1543; G1544; G1548; G1584; G1587; G1588; G1589; G1636; G1642; G1747; G1749; G1749; G1751; G1752; G1763; G1766; G1767; G1778; G1789; G1790; G1791; G1793; G1794; G1795; G1800; G1806; G1811; G1835; G1836; G1838; G1839; G1843; G1853; G1855; G1865; G1881; G1882; G1883; G1884; G1891; G1896; G1898; G1902; G1904; G1906; G1913; G1914; G1925; G1929; G1930; G1954; G1958; G1965; G1976; G2057; G2107; G2133; G2134; G2151; G2154; G2157; G2181;	

		G2290; G2299; G2340; G2340; G2346; G2373; G2376; G2424; G2465; G2505; G2509; G2512; G2513; G2519; G2520; G2533; G2534; G2573; G2589; G2687; G2720; G2787; G2789; G2893	
	Size: increased stature	G189; G1073; G1435; G2430	
	Size: reduced stature or dwarfism	G3; G5; G21; G23; G39; G165; G184; G194; G258; G280; G340; G343; G353; G354; G362; G363; G370; G385; G396; G439; G440; G447; G450; G550; G557; G599; G636; G652; G670; G671; G674; G729; G760; G804; G831; G864; G884; G898; G900; G912; G913; G922; G932; G937; G939; G960; G962; G977; G991; G1000; G1008; G1020; G1023; G1053; G1067; G1075; G1137; G1181; G1198; G1228; G1266; G1267; G1275; G1277; G1309; G1311; G1314; G1317; G1322; G1323; G1326; G1332; G1334; G1367; G1381; G1382; G1386; G1421; G1488; G1494; G1537; G1545; G1560; G1586; G1641; G1652; G1655; G1671; G1750; G1756; G1757; G1782; G1786; G1794; G1839; G1845; G1879; G1886; G1888; G1933; G1939; G1943; G1944; G2011; G2094; G2115;	Ornamental; small stature provides wind resistance; creation of dwarf varieties

		G2130; G2132; G2144; G2145; G2147; G2156; G2294; G2313; G2344; G2431; G2510; G2517; G2521; G2893; G2893	
	Fruit size and number	G362	Biomass, yield, cotton boll fiber density
	Flower structure, inflorescence	G47; G259; G353; G354; G671; G732; G988; G1000; G1063; G1140; G1326; G1449; G1543; G1560; G1587; G1645; G1947; G2108; G2143; G2893	Ornamental horticulture; production of saffron or other edible flowers
	Number and development of trichomes	G225; G226; G247; G362; G585; G634; G676; G682; G1014; G1332; G1452; G1795; G2105	Resistance to pests and desiccation; essential oil production
	Seed size, color, and number	G156; G450; G584; G652; G668; G858; G979; G1040; G1062; G1145; G1255; G1494; G1531; G1534; G1594; G2105; G2114;	Yield
	Root development, modifications	G9; G1482; G1534; G1794; G1852; G2053; G2136; G2140	
	Modifications to root hairs	G225; G226	Nutrient, water uptake, pathogen resistance
	Apical dominance	G559; G732; G1255; G1275; G1411; G1488; G1635; G2452; G2509	Ornamental horticulture
	Branching patterns	G568; G988; G1548	Ornamental horticulture, knot reduction, improved

			windscreen
	Leaf shape, color, modifications	G375; G377; G428; G438; G447; G464; G557; G577; G599; G635; G671; G674; G736; G804; G903; G977; G921; G922; G1038; G1063; G1067; G1073; G1075; G1146; G1152; G1198; G1267; G1269; G1452; G1484; G1586; G1594; G1767; G1786; G1792; G1886; G2059; G2094; G2105; G2113; G2117; G2143; G2144; G2431; G2452; G2465; G2587; G2583; G2724;	Appealing shape or shiny leaves for ornamental agriculture, increased biomass or photosynthesis
	Silique	G1134	Ornamental
	Stem morphology	G47; G438; G671; G748; G988; G1000	Ornamental; digestibility
	Shoot modifications	G390; G391	Ornamental stem bifurcations
Disease, Pathogen Resistance	Bacterial	G211; G347; G367; G418; G525; G545; G578; G1049	Yield, appearance, survivability, extended range
	Fungal	G19; G28; G28; G28; G147; G188; G207; G211; G237; G248; G278; G347; G367; G371; G378; G409; G477; G545; G545; G558; G569; G578; G591; G594; G616; G789; G805; G812; G865; G869; G872; G881; G896; G940; G1047; G1049; G1064; G1084; G1196; G1255; G1266;	Yield, appearance, survivability, extended range

		G1363; G1514; G1756; G1792; G1792; G1792; G1792; G1880; G1919; G1919; G1927; G1927; G1936; G1936; G1950; G2069; G2130; G2380; G2380; G2555	
Nutrients	Increased tolerance to nitrogen-limited soils	G225; G226; G1792	
	Increased tolerance to phosphate-limited soils	G419; G545; G561; G1946	
	Increased tolerance to potassium-limited soils	G561; G911	
Hormonal	Hormone sensitivity	G12; G546; G926; G760; G913; G926; G1062; G1069; G1095; G1134; G1330; G1452; G1666; G1820; G2140; G2789	Seed dormancy, drought tolerance; plant form, fruit ripening
Seed biochemistry	Production of seed prenyl lipids, including tocopherol	G214; G259; G490; G652; G748; G883; G1052; G1328; G1930; G2509; G2520	Antioxidant activity, vitamin E
	Production of seed sterols	G20	Precursors for human steroid hormones; cholesterol modulators
	Production of seed glucosinolates	G353; G484; G674; G1272; G1506; G1897; G1946; G2113; G2117; G2155; G2290; G2340	Defense against insects; putative anticancer activity; undesirable in

			animal feeds
	Modified seed oil content	G162; G162; G180; G192; G241; G265; G286; G291; G427; G509; G519; G561; G567; G590; G818; G849; G892; G961; G974; G1063; G1143; G1190; G1198; G1226; G1229; G1323; G1451; G1471; G1478; G1496; G1526; G1543; G1640; G1644; G1646; G1672; G1677; G1750; G1765; G1777; G1793; G1838; G1902; G1946; G1948; G2059; G2123; G2138; G2139; G2343; G2792; G2830	Vegetable oil production; increased caloric value for animal feeds; lutein content
	Modified seed oil composition	G217; G504; G622; G778; G791; G861; G869; G938; G965; G1417; G2192	Heat stability, digestibility of seed oils
	Modified seed protein content	G162; G226; G241; G371; G427; G509; G567; G597; G732; G849; G865; G892; G963; G988; G1323; G1323; G1419; G1478; G1488; G1634; G1637; G1641; G1644; G1652; G1677; G1777; G1777; G1818; G1820; G1903; G1909; G1946; G1946; G1958; G2059; G2117; G2417; G2509	Reduced caloric value for humans
Leaf biochemistry	Production of flavonoids	G1666*	Ornamental pigment production; pathogen resistance; health

			benefits
	Production of leaf glucosinolates	G264; G353; G484; G652; G674; G681; G1069; G1198; G1322; G1421; G1657; G1794; G1897; G1946; G2115; G2117; G2144; G2155; G2155; G2340; G2512; G2520; G2552	Defense against insects; putative anticancer activity; undesirable in animal feeds
	Production of diterpenes	G229	Induction of enzymes involved in alkaloid biosynthesis
	Production of anthocyanin	G546	Ornamental pigment
	Production of leaf phytosterols, inc. stigmastanol, campesterol	G561; G2131; G2424	Precursors for human steroid hormones; cholesterol modulators
	Leaf fatty acid composition	G214; G377; G861; G962; G975; G987; G1266; G1337; G1399; G1465; G1512; G2136; G2147; G2192	Nutritional value; increase in waxes for disease resistance
	Production of leaf prenyl lipids, including tocopherol	G214; G259; G280; G652; G987; G1543; G2509; G2520	Antioxidant activity, vitamin E
Biochemistry, general	Production of miscellaneous secondary metabolites	G229; G663	
	Sugar, starch, hemicellulose composition,	G158; G211; G211; G237; G242; G274; G598; G1012; G1266; G1309; G1309; G1641; G1765; G1865; G2094; G2094;	Food digestibility, hemicellulose & pectin content; fiber content; plant

		G2589; G2589	tensile strength, wood quality, pathogen resistance, pulp production; tuber starch content
Sugar sensing	Plant response to sugars	G26; G38; G43; G207; G218; G241; G254; G263; G308; G536; G567; G567; G680; G867; G912; G956; G996; G1068; G1225; G1314; G1314; G1337; G1759; G1804; G2153; G2379	Photosynthetic rate, carbohydrate accumulation, biomass production, source-sink relationships, senescence
Growth, Reproduction	Plant growth rate and development	G447; G617; G674; G730; G917; G937; G1035; G1046; G1131; G1425; G1452; G1459; G1492; G1589; G1652; G1879; G1943; G2430; G2431; G2465; G2521	Faster growth, increased biomass or yield, improved appearance; delay in bolting
	Embryo development	G167	
	Seed germination rate	G979; G1792; G2130	Yield
	Plant, seedling vigor	G561; G2346	Survivability, yield
	Senescence; cell death	G571; G636; G878; G1050; G1463; G1749; G1944; G2130; G2155; G2340; G2383	Yield, appearance; response to pathogens;
	Modified fertility	G39; G340; G439; G470; G559; G615; G652; G671; G779; G962; G977; G988; G1000; G1063; G1067; G1075;	Prevents or minimizes escape of the pollen of GMOs

		G1266; G1311; G1321; G1326; G1367; G1386; G1421; G1453; G1471; G1453; G1560; G1594; G1635; G1750; G1947; G2011; G2094; G2113; G2115; G2130; G2143; G2147; G2294; G2510; G2893	
	Early flowering	G147; G157; G180; G183; G183; G184; G185; G208; G227; G294; G390; G390; G390; G391; G391; G427; G427; G490; G565; G590; G592; G720; G789; G865; G898; G898; G989; G989; G1037; G1037; G1142; G1225; G1225; G1226; G1242; G1305; G1305; G1380; G1380; G1480; G1480; G1488; G1494; G1545; G1545; G1649; G1706; G1760; G1767; G1767; G1820; G1841; G1841; G1842; G1843; G1843; G1946; G1946; G2010; G2030; G2030; G2144; G2144; G2295; G2295; G2347; G2348; G2348; G2373; G2373; G2509; G2509; G2555; G2555	Faster generation time; synchrony of flowering; potential for introducing new traits to single variety
	Delayed flowering	G8; G47; G192; G214; G234; G361; G362; G562; G568; G571; G591; G680; G736; G748; G859; G878; G910; G912; G913; G971; G994; G1051; G1052; G1073; G1079; G1335; G1435; G1452; G1478;	Delayed time to pollen production of GMO plants; synchrony of flowering; increased yield

		G1789; G1804; G1865; G1865; G1895; G1900; G2007; G2133; G2155; G2291; G2465	
	Extended flowering phase	G1947	
	Flower and leaf development	G259; G353; G377; G580; G638 G652; G858; G869; G917; G922; G932; G1063; G1075; G1140; G1425; G1452; G1499; G1548; G1645; G1865; G1897; G1933; G2094; G2124; G2140; G2143; G2535; G2557	Ornamental applications; decreased fertility
	Flower abscission	G1897	Ornamental: longer retention of flowers

* When co-expressed with G669 and G663

<u>Significance of modified plant traits</u>

Currently, the existence of a series of maturity groups for different latitudes represents a major barrier to the introduction of new valuable traits. Any trait (e.g. disease resistance) has to be bred into each of the different maturity groups separately, a laborious and costly exercise. The availability of single strain, which could be grown at any latitude, would therefore greatly increase the potential for introducing new traits to crop species such as soybean and cotton.

For many of the traits, listed in Table 6 and below, that may be conferred to plants, a single transcription factor gene may be used to increase or decrease, advance or delay, or improve or prove deleterious to a given trait. For example, overexpression of a transcription factor gene that naturally occurs in a plant may cause early flowering relative to non-transformed or wild-type plants. By knocking out the gene, or suppressing the gene (with, for example, antisense suppression) the plant may experience delayed flowering. Similarly, overexpressing or suppressing one or more genes can impart significant differences in production of plant products,

such as different fatty acid ratios. Thus, suppressing a gene that causes a plant to be more sensitive to cold may improve a plant's tolerance of cold.

Salt stress resistance. Soil salinity is one of the more important variables that determines where a plant may thrive. Salinity is especially important for the successful cultivation of crop plants, particular in many parts of the world that have naturally high soil salt concentrations, or where the soil has been over-utilized. Thus, presently disclosed transcription factor genes that provide increased salt tolerance during germination, the seedling stage, and throughout a plant's life cycle would find particular value for imparting survivability and yield in areas where a particular crop would not normally prosper.

Osmotic stress resistance. Presently disclosed transcription factor genes that confer resistance to osmotic stress may increase germination rate under adverse conditions, which could impact survivability and yield of seeds and plants.

Cold stress resistance. The potential utility of presently disclosed transcription factor genes that increase tolerance to cold is to confer better germination and growth in cold conditions. The germination of many crops is very sensitive to cold temperatures. Genes that would allow germination and seedling vigor in the cold would have highly significant utility in allowing seeds to be planted earlier in the season with a high rate of survivability. Transcription factor genes that confer better survivability in cooler climates allow a grower to move up planting time in the spring and extend the growing season further into autumn for higher crop yields.

Tolerance to freezing. The presently disclosed transcription factor genes that impart tolerance to freezing conditions are useful for enhancing the survivability and appearance of plants conditions or conditions that would otherwise cause extensive cellular damage. Thus, germination of seeds and survival may take place at temperatures significantly below that of the mean temperature required for germination of seeds and survival of non-transformed plants. As with salt tolerance, this has the added benefit of increasing the potential range of a crop plant into regions in which it would otherwise succumb. Cold tolerant transformed plants may also be

planted earlier in the spring or later in autumn, with greater success than with non-transformed plants.

Heat stress tolerance. The germination of many crops is also sensitive to high temperatures. Presently disclosed transcription factor genes that provide increased heat tolerance are generally useful in producing plants that germinate and grow in hot conditions, may find particular use for crops that are planted late in the season, or extend the range of a plant by allowing growth in relatively hot climates.

Drought, low humidity tolerance. Strategies that allow plants to survive in low water conditions may include, for example, reduced surface area or surface oil or wax production. A number of presently disclosed transcription factor genes increase a plant's tolerance to low water conditions and provide the benefits of improved survivability, increased yield and an extended geographic and temporal planting range.

Radiation resistance. Presently disclosed transcription factor genes have been shown to increase lutein production. Lutein, like other xanthophylls such as zeaxanthin and violaxanthin, are important in the protection of plants against the damaging effects of excessive light. Lutein contributes, directly or indirectly, to the rapid rise of non-photochemical quenching in plants exposed to high light. Increased tolerance of field plants to visible and ultraviolet light impacts survivability and vigor, particularly for recent transplants. Also affected are the yield and appearance of harvested plants or plant parts. Crop plants engineered with presently disclosed transcription factor genes that cause the plant to produce higher levels of lutein therefore would have improved photoprotection, leading to less oxidative damage and increase vigor, survivability and higher yields under high light and ultraviolet light conditions.

Decreased herbicide sensitivity. Presently disclosed transcription factor genes that confer resistance or tolerance to herbicides (e.g., glyphosate) may find use in providing means to increase herbicide applications without detriment to desirable plants. This would allow for the increased use of a particular herbicide in a local

environment, with the effect of increased detriment to undesirable species and less harm to transgenic, desirable cultivars.

Increased herbicide sensitivity. Knockouts of a number of the presently disclosed transcription factor genes have been shown to be lethal to developing embryos. Thus, these genes are potentially useful as herbicide targets.

Oxidative stress. In plants, as in all living things, abiotic and biotic stresses induce the formation of oxygen radicals, including superoxide and peroxide radicals. This has the effect of accelerating senescence, particularly in leaves, with the resulting loss of yield and adverse effect on appearance. Generally, plants that have the highest level of defense mechanisms, such as, for example, polyunsaturated moieties of membrane lipids, are most likely to thrive under conditions that introduce oxidative stress (e.g., high light, ozone, water deficit, particularly in combination). Introduction of the presently disclosed transcription factor genes that increase the level of oxidative stress defense mechanisms would provide beneficial effects on the yield and appearance of plants. One specific oxidizing agent, ozone, has been shown to cause significant foliar injury, which impacts yield and appearance of crop and ornamental plants. In addition to reduced foliar injury that would be found in ozone resistant plant created by transforming plants with some of the presently disclosed transcription factor genes, the latter have also been shown to have increased chlorophyll fluorescence (Yu-Sen Chang et al. Bot. Bull. Acad. Sin. (2001) 42: 265-272).

Heavy metal tolerance. Heavy metals such as lead, mercury, arsenic, chromium and others may have a significant adverse impact on plant respiration. Plants that have been transformed with presently disclosed transcription factor genes that confer improved resistance to heavy metals, through, for example, sequestering or reduced uptake of the metals will show improved vigor and yield in soils with relatively high concentrations of these elements. Conversely, transgenic transcription factors may also be introduced into plants to confer an increase in heavy metal uptake, which may benefit efforts to clean up contaminated soils.

Light response. Presently disclosed transcription factor genes that modify a plant's response to light may be useful for modifying a plant's growth or

development, for example, photomorphogenesis in poor light, or accelerating flowering time in response to various light intensities, quality or duration to which a non-transformed plant would not similarly respond. Examples of such responses that have been demonstrated include leaf number and arrangement, and early flower bud appearances.

Overall plant architecture. Several presently disclosed transcription factor genes have been introduced into plants to alter numerous aspects of the plant's morphology. For example, it has been demonstrated that a number of transcription factors may be used to manipulate branching, such as the means to modify lateral branching, a possible application in the forestry industry. Transgenic plants have also been produced that have altered cell wall content, lignin production, flower organ number, or overall shape of the plants. Presently disclosed transcription factor genes transformed into plants may be used to affect plant morphology by increasing or decreasing internode distance, both of which may be advantageous under different circumstances. For example, for fast growth of woody plants to provide more biomass, or fewer knots, increased internode distances are generally desirable. For improved wind screening of shrubs or trees, or harvesting characteristics of, for example, members of the Gramineae family, decreased internode distance may be advantageous. These modifications would also prove useful in the ornamental horticulture industry for the creation of unique phenotypic characteristics of ornamental plants.

Increased stature. For some ornamental plants, the ability to provide larger varieties may be highly desirable. For many plants, including t fruit-bearing trees or trees and shrubs that serve as view or wind screens, increased stature provides obvious benefits. Crop species may also produce higher yields on larger cultivars.

Reduced stature or dwarfism. Presently disclosed transcription factor genes that decrease plant stature can be used to produce plants that are more resistant to damage by wind and rain, or more resistant to heat or low humidity or water deficit. Dwarf plants are also of significant interest to the ornamental horticulture industry, and particularly for home garden applications for which space availability may be limited.

Fruit size and number. Introduction of presently disclosed transcription factor genes that affect fruit size will have desirable impacts on fruit size and number, which may comprise increases in yield for fruit crops, or reduced fruit yield, such as when vegetative growth is preferred (e.g., with bushy ornamentals, or where fruit is undesirable, as with ornamental olive trees).

Flower structure, inflorescence, and development. Presently disclosed transgenic transcription factors have been used to create plants with larger flowers or arrangements of flowers that are distinct from wild-type or non-transformed cultivars. This would likely have the most value for the ornamental horticulture industry, where larger flowers or interesting presentations generally are preferred and command the highest prices. Flower structure may have advantageous effects on fertility, and could be used, for example, to decrease fertility by the absence, reduction or screening of reproductive components. One interesting application for manipulation of flower structure, for example, by introduced transcription factors could be in the increased production of edible flowers or flower parts, including saffron, which is derived from the stigmas of *Crocus sativus*.

Number and development of trichomes. Several presently disclosed transcription factor genes have been used to modify trichome number and amount of trichome products in plants. Trichome glands on the surface of many higher plants produce and secrete exudates that give protection from the elements and pests such as insects, microbes and herbivores. These exudates may physically immobilize insects and spores, may be insecticidal or ant-microbial or they may act as allergens or irritants to protect against herbivores. Trichomes have also been suggested to decrease transpiration by decreasing leaf surface air flow, and by exuding chemicals that protect the leaf from the sun.

Seed size, color and number. The introduction of presently disclosed transcription factor genes into plants that alter the size or number of seeds may have a significant impact on yield, both when the product is the seed itself, or when biomass of the vegetative portion of the plant is increased by reducing seed production. In the case of fruit products, it is often advantageous to modify a plant to have reduced size

or number of seeds relative to non-transformed plants to provide seedless or varieties with reduced numbers or smaller seeds. Presently disclosed transcription factor genes have also been shown to affect seed size, including the development of larger seeds. Seed size, in addition to seed coat integrity, thickness and permeability, seed water content and by a number of other components including antioxidants and oligosaccharides, may affect seed longevity in storage. This would be an important utility when the seed of a plant is the harvested crops, as with, for example, peas, beans, nuts, etc. Presently disclosed transcription factor genes have also been used to modify seed color, which could provide added appeal to a seed product.

Root development, modifications. By modifying the structure or development of roots by transforming into a plant one or more of the presently disclosed transcription factor genes, plants may be produced that have the capacity to thrive in otherwise unproductive soils. For example, grape roots that extend further into rocky soils, or that remain viable in waterlogged soils, would increase the effective planting range of the crop. It may be advantageous to manipulate a plant to produce short roots, as when a soil in which the plant will be growing is occasionally flooded, or when pathogenic fungi or disease-causing nematodes are prevalent.

Modifications to root hairs. Presently disclosed transcription factor genes that increase root hair length or number potentially could be used to increase root growth or vigor, which might in turn allow better plant growth under adverse conditions such as limited nutrient or water availability.

Apical dominance. The modified expression of presently disclosed transcription factors that control apical dominance could be used in ornamental horticulture, for example, to modify plant architecture.

Branching patterns. Several presently disclosed transcription factor genes have been used to manipulate branching, which could provide benefits in the forestry industry. For example, reduction in the formation of lateral branches could reduce knot formation. Conversely, increasing the number of lateral branches could provide utility when a plant is used as a windscreen, or may also provide ornamental advantages.

Leaf shape, color and modifications. It has been demonstrated in laboratory experiments that overexpression of some of the presently disclosed transcription factors produced marked effects on leaf development. At early stages of growth, these transgenic seedlings developed narrow, upward pointing leaves with long petioles, possibly indicating a disruption in circadian-clock controlled processes or nyctinastic movements. Other transcription factor genes can be used to increase plant biomass; large size would be useful in crops where the vegetative portion of the plant is the marketable portion.

Siliques. Genes that later silique conformation in brassicates may be used to modify fruit ripening processes in brassicates and other plants, which may positively affect seed or fruit quality.

Stem morphology and shoot modifications. Laboratory studies have demonstrated that introducing several of the presently disclosed transcription factor genes into plants can cause stem bifurcations in shoots, in which the shoot meristems split to form two or three separate shoots. This unique appearance would be desirable in ornamental applications.

Diseases, pathogens and pests. A number of the presently disclosed transcription factor genes have been shown to or are likely to confer resistance to various plant diseases, pathogens and pests. The offending organisms include fungal *pathogens Fusarium oxysporum, Botrytis cinerea, Sclerotinia sclerotiorum,* and *Erysiphe orontii*. Bacterial pathogens to which resistance may be conferred include *Pseudomonas syringae*. Other problem organisms may potentially include nematodes, mollicutes, parasites, or herbivorous arthropods. In each case, one or more transformed transcription factor genes may provide some benefit to the plant to help prevent or overcome infestation. The mechanisms by which the transcription factors work could include increasing surface waxes or oils, surface thickness, local senescence, or the activation of signal transduction pathways that regulate plant defense in response to attacks by herbivorous pests (including, for example, protease inhibitors).

Increased tolerance of plants to nutrient-limited soils. Presently disclosed transcription factor genes introduced into plants may provide the means to improve uptake of essential nutrients, including nitrogenous compounds, phosphates, potassium, and trace minerals. The effect of these modifications is to increase the seedling germination and range of ornamental and crop plants. The utilities of presently disclosed transcription factor genes conferring tolerance to conditions of low nutrients also include cost savings to the grower by reducing the amounts of fertilizer needed, environmental benefits of reduced fertilizer runoff; and improved yield and stress tolerance. In addition, this gene could be used to alter seed protein amounts and/or composition that could impact yield as well as the nutritional value and production of various food products.

Hormone sensitivity. One or more of the presently disclosed transcription factor genes have been shown to affect plant abscisic acid (ABA) sensitivity. This plant hormone is likely the most important hormone in mediating the adaptation of a plant to stress. For example, ABA mediates conversion of apical meristems into dormant buds. In response to increasingly cold conditions, the newly developing leaves growing above the meristem become converted into stiff bud scales that closely wrap the meristem and protect it from mechanical damage during winter. ABA in the bud also enforces dormancy; during premature warm spells, the buds are inhibited from sprouting. Bud dormancy is eliminated after either a prolonged cold period of cold or a significant number of lengthening days. Thus, by affecting ABA sensitivity, introduced transcription factor genes may affect cold sensitivity and survivability. ABA is also important in protecting plants from drought tolerance.

Several other of the present transcription factor genes have been used to manipulate ethylene signal transduction and response pathways. These genes can thus be used to manipulate the processes influenced by ethylene, such as seed germination or fruit ripening, and to improve seed or fruit quality.

Production of seed and leaf prenyl lipids, including tocopherol. Prenyl lipids play a role in anchoring proteins in membranes or membranous organelles. Thus modifying the prenyl lipid content of seeds and leaves could affect membrane integrity and function. A number of presently disclosed transcription factor genes

have been shown to modify the tocopherol composition of plants. Tocopherols have both anti-oxidant and vitamin E activity.

Production of seed and leaf phytosterols: Presently disclosed transcription factor genes that modify levels of phytosterols in plants may have at least two utilities. First, phytosterols are an important source of precursors for the manufacture of human steroid hormones. Thus, regulation of transcription factor expression or activity could lead to elevated levels of important human steroid precursors for steroid semi-synthesis. For example, transcription factors that cause elevated levels of campesterol in leaves, or sitosterols and stigmasterols in seed crops, would be useful for this purpose. Phytosterols and their hydrogenated derivatives phytostanols also have proven cholesterol-lowering properties, and transcription factor genes that modify the expression of these compounds in plants would thus provide health benefits.

Production of seed and leaf glucosinolates. Some glucosinolates have anti-cancer activity; thus, increasing the levels or composition of these compounds by introducing several of the presently disclosed transcription factors might be of interest from a nutraceutical standpoint. (3) Glucosinolates form part of a plants natural defense against insects. Modification of glucosinolate composition or quantity could therefore afford increased protection from predators. Furthermore, in edible crops, tissue specific promoters might be used to ensure that these compounds accumulate specifically in tissues, such as the epidermis, which are not taken for consumption.

Modified seed oil content. The composition of seeds, particularly with respect to seed oil amounts and/or composition, is very important for the nutritional value and production of various food and feed products. Several of the presently disclosed transcription factor genes in seed lipid saturation that alter seed oil content could be used to improve the heat stability of oils or to improve the nutritional quality of seed oil, by, for example, reducing the number of calories in seed, increasing the number of calories in animal feeds, or altering the ratio of saturated to unsaturated lipids comprising the oils.

Seed and leaf fatty acid composition. A number of the presently disclosed transcription factor genes have been shown to alter the fatty acid composition in plants, and seeds in particular. This modification may find particular value for improving the nutritional value of, for example, seeds or whole plants. Dietary fatty acids ratios have been shown to have an effect on, for example, bone integrity and remodeling (see, for example, Weiler, H.A., *Pediatr Res* (2000) 47:5 692-697). The ratio of dietary fatty acids may alter the precursor pools of long-chain polyunsaturated fatty acids that serve as precursors for prostaglandin synthesis. In mammalian connective tissue, prostaglandins serve as important signals regulating the balance between resorption and formation in bone and cartilage. Thus dietary fatty acid ratios altered in seeds may affect the etiology and outcome of bone loss.

Modified seed protein content. As with seed oils, the composition of seeds, particularly with respect to protein amounts and/or composition, is very important for the nutritional value and production of various food and feed products. A number of the presently disclosed transcription factor genes modify the protein concentrations in seeds would provide nutritional benefits, and may be used to prolong storage, increase seed pest or disease resistance, or modify germination rates.

Production of flavonoids in leaves and other plant parts. Expression of presently disclosed transcription factor genes that increase flavonoid production in plants, including anthocyanins and condensed tannins, may be used to alter in pigment production for horticultural purposes, and possibly increasing stress resistance. Flavonoids have antimicrobial activity and could be used to engineer pathogen resistance. Several flavonoid compounds have health promoting effects such as the inhibition of tumor growth and cancer, prevention of bone loss and the prevention of the oxidation of lipids. Increasing levels of condensed tannins, whose biosynthetic pathway is shared with anthocyanin biosynthesis, in forage legumes is an important agronomic trait because they prevent pasture bloat by collapsing protein foams within the rumen. For a review on the utilities of flavonoids and their derivatives, refer to Dixon et al. (1999) Trends Plant Sci. 4:394-400.

Production of diterpenes in leaves and other plant parts. Depending on the plant species, varying amounts of diverse secondary biochemicals (often lipophilic

terpenes) are produced and exuded or volatilized by trichomes. These exotic secondary biochemicals, which are relatively easy to extract because they are on the surface of the leaf, have been widely used in such products as flavors and aromas, drugs, pesticides and cosmetics. Thus, the overexpression of genes that are used to produce diterpenes in plants may be accomplished by introducing transcription factor genes that induce said overexpression. One class of secondary metabolites, the diterpenes, can effect several biological systems such as tumor progression, prostaglandin synthesis and tissue inflammation. In addition, diterpenes can act as insect pheromones, termite allomones, and can exhibit neurotoxic, cytotoxic and antimitotic activities. As a result of this functional diversity, diterpenes have been the target of research several pharmaceutical ventures. In most cases where the metabolic pathways are impossible to engineer, increasing trichome density or size on leaves may be the only way to increase plant productivity.

Production of anthocyanin in leaves and other plant parts. Several presently disclosed transcription factor genes can be used to alter anthocyanin production in numerous plant species. The potential utilities of these genes include alterations in pigment production for horticultural purposes, and possibly increasing stress resistance in combination with another transcription factor.

Production of miscellaneous secondary metabolites. Microarray data suggests that flux through the aromatic amino acid biosynthetic pathways and primary and secondary metabolite biosynthetic pathways are up-regulated. Presently disclosed transcription factors have been shown to be involved in regulating alkaloid biosynthesis, in part by up-regulating the enzymes indole-3-glycerol phosphatase and strictosidine synthase. Phenylalanine ammonia lyase, chalcone synthase and trans-cinnamate mono-oxygenase are also induced, and are involved in phenylpropenoid biosynthesis.

Sugar, starch, hemicellulose composition. Overexpression of the presently disclosed transcription factors that affect sugar content resulted in plants with altered leaf insoluble sugar content. Transcription factors that alter plant cell wall composition have several potential applications including altering food digestibility, plant tensile strength, wood quality, pathogen resistance and in pulp production. The

potential utilities of a gene involved in glucose-specific sugar sensing are to alter energy balance, photosynthetic rate, carbohydrate accumulation, biomass production, source-sink relationships, and senescence.

Hemicellulose is not desirable in paper pulps because of its lack of strength compared with cellulose. Thus modulating the amounts of cellulose vs. hemicellulose in the plant cell wall is desirable for the paper/lumber industry. Increasing the insoluble carbohydrate content in various fruits, vegetables, and other edible consumer products will result in enhanced fiber content. Increased fiber content would not only provide health benefits in food products, but might also increase digestibility of forage crops. In addition, the hemicellulose and pectin content of fruits and berries affects the quality of jam and catsup made from them. Changes in hemicellulose and pectin content could result in a superior consumer product.

Plant response to sugars and sugar composition. In addition to their important role as an energy source and structural component of the plant cell, sugars are central regulatory molecules that control several aspects of plant physiology, metabolism and development. It is thought that this control is achieved by regulating gene expression and, in higher plants, sugars have been shown to repress or activate plant genes involved in many essential processes such as photosynthesis, glyoxylate metabolism, respiration, starch and sucrose synthesis and degradation, pathogen response, wounding response, cell cycle regulation, pigmentation, flowering and senescence. The mechanisms by which sugars control gene expression are not understood.

Because sugars are important signaling molecules, the ability to control either the concentration of a signaling sugar or how the plant perceives or responds to a signaling sugar could be used to control plant development, physiology or metabolism. For example, the flux of sucrose (a disaccharide sugar used for systemically transporting carbon and energy in most plants) has been shown to affect gene expression and alter storage compound accumulation in seeds. Manipulation of the sucrose signaling pathway in seeds may therefore cause seeds to have more protein, oil or carbohydrate, depending on the type of manipulation. Similarly, in tubers, sucrose is converted to starch which is used as an energy store. It is thought that sugar signaling pathways may partially determine the levels of starch synthesized

in the tubers. The manipulation of sugar signaling in tubers could lead to tubers with a higher starch content.

Thus, the presently disclosed transcription factor genes that manipulate the sugar signal transduction pathway may lead to altered gene expression to produce plants with desirable traits. In particular, manipulation of sugar signal transduction pathways could be used to alter source-sink relationships in seeds, tubers, roots and other storage organs leading to increase in yield.

Plant growth rate and development. A number of the presently disclosed transcription factor genes have been shown to have significant effects on plant growth rate and development. These observations have included, for example, more rapid or delayed growth and development of reproductive organs. This would provide utility for regions with short or long growing seasons, respectively. Accelerating plant growth would also improve early yield or increase biomass at an earlier stage, when such is desirable (for example, in producing forestry products).

Embryo development. Presently disclosed transcription factor genes that alter embryo development has been used to alter seed protein and oil amounts and/or composition which is very important for the nutritional value and production of various food products. Seed shape and seed coat may also be altered by these genes, which may provide for improved storage stability.

Seed germination rate. A number of the presently disclosed transcription factor genes have been shown to modify seed germination rate, including when the seeds are in conditions normally unfavorable for germination (e.g., cold, heat or salt stress, or in the presence of ABA), and may thus be used to modify and improve germination rates under adverse conditions.

Plant, seedling vigor. Seedlings transformed with presently disclosed transcription factors have been shown to possess larger cotyledons and appeared somewhat more advanced than control plants. This indicates that the seedlings developed more rapidly that the control plants. Rapid seedling development is likely to reduce loss due to diseases particularly prevalent at the seedling stage (e.g.,

damping off) and is thus important for survivability of plants germinating in the field or in controlled environments.

Senescence, cell death. Presently disclosed transcription factor genes may be used to alter senescence responses in plants. Although leaf senescence is thought to be an evolutionary adaptation to recycle nutrients, the ability to control senescence in an agricultural setting has significant value. For example, a delay in leaf senescence in some maize hybrids is associated with a significant increase in yields and a delay of a few days in the senescence of soybean plants can have a large impact on yield. Delayed flower senescence may also generate plants that retain their blossoms longer and this may be of potential interest to the ornamental horticulture industry.

Modified fertility. Plants that overexpress a number of the presently disclosed transcription factor genes have been shown to possess reduced fertility. This could be a desirable trait, as it could be exploited to prevent or minimize the escape of the pollen of genetically modified organisms (GMOs) into the environment.

Early and delayed flowering. Presently disclosed transcription factor genes that accelerate flowering could have valuable applications in such programs since they allow much faster generation times. In a number of species, for example, broccoli, cauliflower, where the reproductive parts of the plants constitute the crop and the vegetative tissues are discarded, it would be advantageous to accelerate time to flowering. Accelerating flowering could shorten crop and tree breeding programs. Additionally, in some instances, a faster generation time might allow additional harvests of a crop to be made within a given growing season. A number of *Arabidopsis* genes have already been shown to accelerate flowering when constitutively expressed. These include LEAFY, APETALA1 and CONSTANS (Mandel, M. et al., 1995, Nature 377, 522-524; Weigel, D. and Nilsson, O., 1995, Nature 377, 495-500; Simon et al., 1996, Nature 384, 59-62).

By regulating the expression of potential flowering using inducible promoters, flowering could be triggered by application of an inducer chemical. This would allow flowering to be synchronized across a crop and facilitate more efficient harvesting. Such inducible systems could also be used to tune the flowering of crop varieties to

different latitudes. At present, species such as soybean and cotton are available as a series of maturity groups that are suitable for different latitudes on the basis of their flowering time (which is governed by day-length). A system in which flowering could be chemically controlled would allow a single high-yielding northern maturity group to be grown at any latitude. In southern regions such plants could be grown for longer, thereby increasing yields, before flowering was induced. In more northern areas, the induction would be used to ensure that the crop flowers prior to the first winter frosts.

In a sizeable number of species, for example, root crops, where the vegetative parts of the plants constitute the crop and the reproductive tissues are discarded, it would be advantageous to delay or prevent flowering. Extending vegetative development with presently disclosed transcription factor genes could thus bring about large increases in yields.. Prevention of flowering might help maximize vegetative yields and prevent escape of genetically modified organism (GMO) pollen.

Extended flowering phase. Presently disclosed transcription factors that extend flowering time have utility in engineering plants with longer-lasting flowers for the horticulture industry, and for extending the time in which the plant is fertile.

Flower and leaf development. Presently disclosed transcription factor genes have been used to modify the development of flowers and leaves. This could be advantageous in the development of new ornamental cultivars that present unique configurations. In addition, some of these genes have been shown to reduce a plant's fertility, which is also useful for helping to prevent development of pollen of GMOs.

Flower abscission. Presently disclosed transcription factor genes introduced into plants have been used to retain flowers for longer periods. This would provide a significant benefit to the ornamental industry, for both cut flowers and woody plant varieties (of, for example, maize), as well as have the potential to lengthen the fertile period of a plant, which could positively impact yield and breeding programs.

A listing of specific effects and utilities that the presently disclosed transcription factor genes have on plants, as determined by direct observation and assay analysis, is provided in Table 4.

XVI. Antisense and Co-suppression

In addition to expression of the nucleic acids of the invention as gene replacement or plant phenotype modification nucleic acids, the nucleic acids are also useful for sense and anti-sense suppression of expression, e.g., to down-regulate expression of a nucleic acid of the invention, e.g., as a further mechanism for modulating plant phenotype. That is, the nucleic acids of the invention, or subsequences or anti-sense sequences thereof, can be used to block expression of naturally occurring homologous nucleic acids. A variety of sense and anti-sense technologies are known in the art, e.g., as set forth in Lichtenstein and Nellen (1997) Antisense Technology: A Practical Approach IRL Press at Oxford University Press, Oxford, U.K.. In general, sense or anti-sense sequences are introduced into a cell, where they are optionally amplified, e.g., by transcription. Such sequences include both simple oligonucleotide sequences and catalytic sequences such as ribozymes.

For example, a reduction or elimination of expression (i.e., a "knock-out") of a transcription factor or transcription factor homologue polypeptide in a transgenic plant, e.g., to modify a plant trait, can be obtained by introducing an antisense construct corresponding to the polypeptide of interest as a cDNA. For antisense suppression, the transcription factor or homologue cDNA is arranged in reverse orientation (with respect to the coding sequence) relative to the promoter sequence in the expression vector. The introduced sequence need not be the full length cDNA or gene, and need not be identical to the cDNA or gene found in the plant type to be transformed. Typically, the antisense sequence need only be capable of hybridizing to the target gene or RNA of interest. Thus, where the introduced sequence is of shorter length, a higher degree of homology to the endogenous transcription factor sequence will be needed for effective antisense suppression. While antisense sequences of various lengths can be utilized, preferably, the introduced antisense sequence in the vector will be at least 30 nucleotides in length, and improved antisense suppression will typically be observed as the length of the antisense sequence increases. Preferably, the length of the antisense sequence in the vector will be greater than 100 nucleotides.

Transcription of an antisense construct as described results in the production of RNA molecules that are the reverse complement of mRNA molecules transcribed from the endogenous transcription factor gene in the plant cell.

Suppression of endogenous transcription factor gene expression can also be achieved using a ribozyme. Ribozymes are RNA molecules that possess highly specific endoribonuclease activity. The production and use of ribozymes are disclosed in U.S. Patent No. 4,987,071 and U.S. Patent No. 5,543,508. Synthetic ribozyme sequences including antisense RNAs can be used to confer RNA cleaving activity on the antisense RNA, such that endogenous mRNA molecules that hybridize to the antisense RNA are cleaved, which in turn leads to an enhanced antisense inhibition of endogenous gene expression.

Suppression of endogenous transcription factor gene expression can also be achieved using RNA interference , or RNAi. RNAi is a post-transcriptional, targeted gene-silencing technique that uses double-stranded RNA (dsRNA) to incite degradation of messenger RNA (mRNA) containing the same sequence as the dsRNA (Constans, (2002*) The Scientist* 16:36). Small interfering RNAs, or siRNAs are produced in at least two steps: an endogenous ribonuclease cleaves longer dsRNA into shorter, 21-23 nucleotide-long RNAs. The siRNA segments then mediate the degradation of the target mRNA (Zamore, (2001) *Nature Struct. Biol.*, 8:746-50). RNAi has been used for gene function determination in a manner similar to antisense oligonucleotides (Constans, (2002*) The Scientist* 16:36). Expression vectors that continually express siRNAs in transiently and stably transfected have been engineered to express small hairpin RNAs (shRNAs), which get processed in vivo into siRNAs-like molecules capable of carrying out gene-specific silencing (Brummelkamp et al., (2002) *Science* 296:550-553, and Paddison, et al. (2002) *Genes & Dev.* 16:948-958). Post-transcriptional gene silencing by double-stranded RNA is discussed in further detail by Hammond et al. (2001) *Nature Rev Gen* 2: 110-119, Fire et al. (1998) *Nature* 391: 806-811 and Timmons and Fire (1998) *Nature* 395: 854.

Vectors in which RNA encoded by a transcription factor or transcription factor homologue cDNA is over-expressed can also be used to obtain co-suppression of a corresponding endogenous gene, e.g., in the manner described in U.S. Patent No.

5,231,020 to Jorgensen. Such co-suppression (also termed sense suppression) does not require that the entire transcription factor cDNA be introduced into the plant cells, nor does it require that the introduced sequence be exactly identical to the endogenous transcription factor gene of interest. However, as with antisense suppression, the suppressive efficiency will be enhanced as specificity of hybridization is increased, e.g., as the introduced sequence is lengthened, and/or as the sequence similarity between the introduced sequence and the endogenous transcription factor gene is increased.

Vectors expressing an untranslatable form of the transcription factor mRNA, e.g., sequences comprising one or more stop codon, or nonsense mutation) can also be used to suppress expression of an endogenous transcription factor, thereby reducing or eliminating it's activity and modifying one or more traits. Methods for producing such constructs are described in U.S. Patent No. 5,583,021. Preferably, such constructs are made by introducing a premature stop codon into the transcription factor gene. Alternatively, a plant trait can be modified by gene silencing using double-strand RNA (Sharp (1999) Genes and Development 13: 139-141).Another method for abolishing the expression of a gene is by insertion mutagenesis using the T-DNA of *Agrobacterium tumefaciens*. After generating the insertion mutants, the mutants can be screened to identify those containing the insertion in a transcription factor or transcription factor homologue gene. Plants containing a single transgene insertion event at the desired gene can be crossed to generate homozygous plants for the mutation. Such methods are well known to those of skill in the art. (See for example Koncz et al. (1992) Methods in Arabidopsis Research, World Scientific.)

Alternatively, a plant phenotype can be altered by eliminating an endogenous gene, such as a transcription factor or transcription factor homologue, e.g., by homologous recombination (Kempin et al. (1997) Nature 389:802-803).

A plant trait can also be modified by using the Cre-lox system (for example, as described in US Pat. No. 5,658,772). A plant genome can be modified to include first and second lox sites that are then contacted with a Cre recombinase. If the lox sites are in the same orientation, the intervening DNA sequence between the two sites

is excised. If the lox sites are in the opposite-orientation, the intervening sequence is inverted.

The polynucleotides and polypeptides of this invention can also be expressed in a plant in the absence of an expression cassette by manipulating the activity or expression level of the endogenous gene by other means. For example, by ectopically expressing a gene by T-DNA activation tagging (Ichikawa et al. (1997) Nature 390 698-701; Kakimoto et al. (1996) Science 274: 982-985). This method entails transforming a plant with a gene tag containing multiple transcriptional enhancers and once the tag has inserted into the genome, expression of a flanking gene coding sequence becomes deregulated. In another example, the transcriptional machinery in a plant can be modified so as to increase transcription levels of a polynucleotide of the invention (*See*, e.g., PCT Publications WO 96/06166 and WO 98/53057 which describe the modification of the DNA-binding specificity of zinc finger proteins by changing particular amino acids in the DNA-binding motif).

The transgenic plant can also include the machinery necessary for expressing or altering the activity of a polypeptide encoded by an endogenous gene, for example by altering the phosphorylation state of the polypeptide to maintain it in an activated state.

Transgenic plants (or plant cells, or plant explants, or plant tissues) incorporating the polynucleotides of the invention and/or expressing the polypeptides of the invention can be produced by a variety of well established techniques as described above. Following construction of a vector, most typically an expression cassette, including a polynucleotide, e.g., encoding a transcription factor or transcription factor homologue, of the invention, standard techniques can be used to introduce the polynucleotide into a plant, a plant cell, a plant explant or a plant tissue of interest. Optionally, the plant cell, explant or tissue can be regenerated to produce a transgenic plant.

The plant can be any higher plant, including gymnosperms, monocotyledonous and dicotyledenous plants. Suitable protocols are available for *Leguminosae* (alfalfa, soybean, clover, etc.), *Umbelliferae* (carrot, celery, parsnip),

Cruciferae (cabbage, radish, rapeseed, broccoli, etc.), *Curcurbitaceae* (melons and cucumber), *Gramineae* (wheat, corn, rice, barley, millet, etc.), *Solanaceae* (potato, tomato, tobacco, peppers, etc.), and various other crops. See protocols described in Ammirato et al. (1984) Handbook of Plant Cell Culture –Crop Species, Macmillan Publ. Co. Shimamoto et al. (1989) Nature 338:274-276; Fromm et al. (1990) Bio/Technology 8:833-839; and Vasil et al. (1990) Bio/Technology 8:429-434.

Transformation and regeneration of both monocotyledonous and dicotyledonous plant cells is now routine, and the selection of the most appropriate transformation technique will be determined by the practitioner. The choice of method will vary with the type of plant to be transformed; those skilled in the art will recognize the suitability of particular methods for given plant types. Suitable methods can include, but are not limited to: electroporation of plant protoplasts; liposome-mediated transformation; polyethylene glycol (PEG) mediated transformation; transformation using viruses; micro-injection of plant cells; micro-projectile bombardment of plant cells; vacuum infiltration; and *Agrobacterium tumefaciens* mediated transformation. Transformation means introducing a nucleotide sequence into a plant in a manner to cause stable or transient expression of the sequence.

Successful examples of the modification of plant characteristics by transformation with cloned sequences which serve to illustrate the current knowledge in this field of technology, and which are herein incorporated by reference, include: U.S. Patent Nos. 5,571,706; 5,677,175; 5,510,471; 5,750,386; 5,597,945; 5,589,615; 5,750,871; 5,268,526; 5,780,708; 5,538,880; 5,773,269; 5,736,369 and 5,610,042.

Following transformation, plants are preferably selected using a dominant selectable marker incorporated into the transformation vector. Typically, such a marker will confer antibiotic or herbicide resistance on the transformed plants, and selection of transformants can be accomplished by exposing the plants to appropriate concentrations of the antibiotic or herbicide.

After transformed plants are selected and grown to maturity, those plants showing a modified trait are identified. The modified trait can be any of those traits described above. Additionally, to confirm that the modified trait is due to changes in

expression levels or activity of the polypeptide or polynucleotide of the invention can be determined by analyzing mRNA expression using Northern blots, RT-PCR or microarrays, or protein expression using immunoblots or Western blots or gel shift assays.

XVII. Integrated Systems – Sequence Identity

Additionally, the present invention may be an integrated system, computer or computer readable medium that comprises an instruction set for determining the identity of one or more sequences in a database. In addition, the instruction set can be used to generate or identify sequences that meet any specified criteria. Furthermore, the instruction set may be used to associate or link certain functional benefits, such improved characteristics, with one or more identified sequence.

For example, the instruction set can include, e.g., a sequence comparison or other alignment program, e.g., an available program such as, for example, the Wisconsin Package Version 10.0, such as BLAST, FASTA, PILEUP, FINDPATTERNS or the like (GCG, Madison, WI). Public sequence databases such as GenBank, EMBL, Swiss-Prot and PIR or private sequence databases such as PHYTOSEQ sequence database (Incyte Genomics, Palo Alto, CA) can be searched.

Alignment of sequences for comparison can be conducted by the local homology algorithm of Smith and Waterman (1981) Adv. Appl. Math. 2:482, by the homology alignment algorithm of Needleman and Wunsch (1970) J. Mol. Biol. 48:443-453, by the search for similarity method of Pearson and Lipman (1988) Proc. Natl. Acad. Sci. U.S.A. 85:2444-2448, by computerized implementations of these algorithms. After alignment, sequence comparisons between two (or more) polynucleotides or polypeptides are typically performed by comparing sequences of the two sequences over a comparison window to identify and compare local regions of sequence similarity. The comparison window can be a segment of at least about 20 contiguous positions, usually about 50 to about 200, more usually about 100 to about 150 contiguous positions. A description of the method is provided in Ausubel et al., *supra*.

A variety of methods for determining sequence relationships can be used, including manual alignment and computer assisted sequence alignment and analysis. This later approach is a preferred approach in the present invention, due to the increased throughput afforded by computer assisted methods. As noted above, a variety of computer programs for performing sequence alignment are available, or can be produced by one of skill.

One example algorithm that is suitable for determining percent sequence identity and sequence similarity is the BLAST algorithm, which is described in Altschul et al. J. Mol. Biol 215:403-410 (1990). Software for performing BLAST analyses is publicly available, e.g., through the National Center for Biotechnology Information (see internet website at ncbi.nlm.nih.gov). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul et al., *supra*). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are then extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, a cutoff of 100, M=5, N=-4, and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength (W) of 3, an expectation (E) of 10, and the BLOSUM62 scoring matrix (*see* Henikoff & Henikoff (1989) Proc. Natl. Acad. Sci. USA 89:10915). Unless otherwise indicated, "sequence identity" here refers to the % sequence identity generated from a tblastx using the NCBI version of

the algorithm at the default settings using gapped alignments with the filter "off" (see, for example, internet website at ncbi.nlm.nih.gov).

In addition to calculating percent sequence identity, the BLAST algorithm also performs a statistical analysis of the similarity between two sequences (*see,* e.g., Karlin & Altschul (1993) Proc. Natl. Acad. Sci. USA 90:5873-5787). One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a nucleic acid is considered similar to a reference sequence (and, therefore, in this context, homologous) if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.1, or less than about 0.01, and or even less than about 0.001. An additional example of a useful sequence alignment algorithm is PILEUP. PILEUP creates a multiple sequence alignment from a group of related sequences using progressive, pairwise alignments. The program can align, e.g., up to 300 sequences of a maximum length of 5,000 letters.

The integrated system, or computer typically includes a user input interface allowing a user to selectively view one or more sequence records corresponding to the one or more character strings, as well as an instruction set which aligns the one or more character strings with each other or with an additional character string to identify one or more region of sequence similarity. The system may include a link of one or more character strings with a particular phenotype or gene function. Typically, the system includes a user readable output element that displays an alignment produced by the alignment instruction set.

The methods of this invention can be implemented in a localized or distributed computing environment. In a distributed environment, the methods may implemented on a single computer comprising multiple processors or on a multiplicity of computers. The computers can be linked, e.g. through a common bus, but more preferably the computer(s) are nodes on a network. The network can be a generalized or a dedicated local or wide-area network and, in certain preferred embodiments, the computers may be components of an intra-net or an internet.

Thus, the invention provides methods for identifying a sequence similar or homologous to one or more polynucleotides as noted herein, or one or more target polypeptides encoded by the polynucleotides, or otherwise noted herein and may include linking or associating a given plant phenotype or gene function with a sequence. In the methods, a sequence database is provided (locally or across an inter or intra net) and a query is made against the sequence database using the relevant sequences herein and associated plant phenotypes or gene functions.

Any sequence herein can be entered into the database, before or after querying the database. This provides for both expansion of the database and, if done before the querying step, for insertion of control sequences into the database. The control sequences can be detected by the query to ensure the general integrity of both the database and the query. As noted, the query can be performed using a web browser based interface. For example, the database can be a centralized public database such as those noted herein, and the querying can be done from a remote terminal or computer across an internet or intranet.

XVIII. Examples

The following examples are intended to illustrate but not limit the present invention. The complete descriptions of the traits associated with each polynucleotide of the invention is fully disclosed in Table 4 and Table 6.

Example I: Full Length Gene Identification and Cloning

Putative transcription factor sequences (genomic or ESTs) related to known transcription factors were identified in the *Arabidopsis thaliana* GenBank database using the tblastn sequence analysis program using default parameters and a P-value cutoff threshold of –4 or –5 or lower, depending on the length of the query sequence. Putative transcription factor sequence hits were then screened to identify those containing particular sequence strings. If the sequence hits contained such sequence strings, the sequences were confirmed as transcription factors.

Alternatively, *Arabidopsis thaliana* cDNA libraries derived from different tissues or treatments, or genomic libraries were screened to identify novel members of a transcription family using a low stringency hybridization approach. Probes were

synthesized using gene specific primers in a standard PCR reaction (annealing temperature 60° C) and labeled with ^{32}P dCTP using the High Prime DNA Labeling Kit (Boehringer Mannheim). Purified radiolabelled probes were added to filters immersed in Church hybridization medium (0.5 M $NaPO_4$ pH 7.0, 7% SDS, 1 % w/v bovine serum albumin) and hybridized overnight at 60°C with shaking. Filters were washed two times for 45 to 60 minutes with 1xSCC, 1% SDS at 60° C.

To identify additional sequence 5' or 3' of a partial cDNA sequence in a cDNA library, 5' and 3' rapid amplification of cDNA ends (RACE) was performed using the U.C. Marathon cDNA amplification kit (Clontech, Palo Alto, CA). Generally, the method entailed first isolating poly(A) mRNA, performing first and second strand cDNA synthesis to generate double stranded cDNA, blunting cDNA ends, followed by ligation of the U.C. Marathon Adaptor to the cDNA to form a library of adaptor-ligated ds cDNA.

Gene-specific primers were designed to be used along with adaptor specific primers for both 5' and 3' RACE reactions. Nested primers, rather than single primers, were used to increase PCR specificity. Using 5' and 3' RACE reactions, 5' and 3' RACE fragments were obtained, sequenced and cloned. The process can be repeated until 5' and 3' ends of the full-length gene were identified. Then the full-length cDNA was generated by PCR using primers specific to 5' and 3' ends of the gene by end-to-end PCR.

Example II: Construction of Expression Vectors

The sequence was amplified from a genomic or cDNA library using primers specific to sequences upstream and downstream of the coding region. The expression vector was pMEN20 or pMEN65, which are both derived from pMON316 (Sanders et al, (1987) Nucleic Acids Research 15:1543-1558) and contain the CaMV 35S promoter to express transgenes. To clone the sequence into the vector, both pMEN20 and the amplified DNA fragment were digested separately with SalI and NotI restriction enzymes at 37° C for 2 hours. The digestion products were subject to electrophoresis in a 0.8% agarose gel and visualized by ethidium bromide staining. The DNA fragments containing the sequence and the linearized plasmid were excised and purified by using a Qiaquick gel extraction kit (Qiagen, Valencia CA). The

fragments of interest were ligated at a ratio of 3:1 (vector to insert). Ligation reactions using T4 DNA ligase (New England Biolabs, Beverly MA) were carried out at 16° C for 16 hours. The ligated DNAs were transformed into competent cells of the *E. coli* strain DH5alpha by using the heat shock method. The transformations were plated on LB plates containing 50 mg/l kanamycin (Sigma, St. Louis, MO). Individual colonies were grown overnight in five milliliters of LB broth containing 50 mg/l kanamycin at 37° C. Plasmid DNA was purified by using Qiaquick Mini Prep kits (Qiagen).

Example III: Transformation of *Agrobacterium* with the Expression Vector

After the plasmid vector containing the gene was constructed, the vector was used to transform *Agrobacterium tumefaciens* cells expressing the gene products. The stock of *Agrobacterium tumefaciens* cells for transformation were made as described by Nagel et al. (1990) FEMS Microbiol Letts. 67: 325-328. *Agrobacterium* strain ABI was grown in 250 ml LB medium (Sigma) overnight at 28°C with shaking until an absorbance (A_{600}) of 0.5 – 1.0 was reached. Cells were harvested by centrifugation at 4,000 x g for 15 min at 4° C. Cells were then resuspended in 250 μl chilled buffer (1 mM HEPES, pH adjusted to 7.0 with KOH). Cells were centrifuged again as described above and resuspended in 125 μl chilled buffer. Cells were then centrifuged and resuspended two more times in the same HEPES buffer as described above at a volume of 100 μl and 750 μl, respectively. Resuspended cells were then distributed into 40 μl aliquots, quickly frozen in liquid nitrogen, and stored at -80° C.

Agrobacterium cells were transformed with plasmids prepared as described above following the protocol described by Nagel et al. For each DNA construct to be transformed, 50 – 100 ng DNA (generally resuspended in 10 mM Tris-HCl, 1 mM EDTA, pH 8.0) was mixed with 40 μl of *Agrobacterium* cells. The DNA/cell mixture was then transferred to a chilled cuvette with a 2mm electrode gap and subject to a 2.5 kV charge dissipated at 25 μF and 200 μF using a Gene Pulser II apparatus (Bio-Rad, Hercules, CA). After electroporation, cells were immediately resuspended in 1.0 ml LB and allowed to recover without antibiotic selection for 2 – 4 hours at 28° C in a shaking incubator. After recovery, cells were plated onto selective medium of LB broth containing 100 μg/ml spectinomycin (Sigma) and incubated for 24-48 hours at 28° C. Single colonies were then picked and inoculated in fresh medium. The

presence of the plasmid construct was verified by PCR amplification and sequence analysis.

Example IV: Transformation of *Arabidopsis* Plants with *Agrobacterium tumefaciens* with Expression Vector

After transformation of *Agrobacterium tumefaciens* with plasmid vectors containing the gene, single *Agrobacterium* colonies were identified, propagated, and used to transform *Arabidopsis* plants. Briefly, 500 ml cultures of LB medium containing 50 mg/l kanamycin were inoculated with the colonies and grown at 28° C with shaking for 2 days until an optical absorbance at 600 nm wavelength over 1 cm (A_{600}) of > 2.0 is reached. Cells were then harvested by centrifugation at 4,000 x g for 10 min, and resuspended in infiltration medium (1/2 X Murashige and Skoog salts (Sigma), 1 X Gamborg's B-5 vitamins (Sigma), 5.0% (w/v) sucrose (Sigma), 0.044 μM benzylamino purine (Sigma), 200 μl/l Silwet L-77 (Lehle Seeds) until an A_{600} of 0.8 was reached.

Prior to transformation, *Arabidopsis thaliana* seeds (ecotype Columbia) were sown at a density of ~10 plants per 4" pot onto Pro-Mix BX potting medium (Hummert International) covered with fiberglass mesh (18 mm X 16 mm). Plants were grown under continuous illumination (50-75 $\mu E/m^2/sec$) at 22-23° C with 65-70% relative humidity. After about 4 weeks, primary inflorescence stems (bolts) are cut off to encourage growth of multiple secondary bolts. After flowering of the mature secondary bolts, plants were prepared for transformation by removal of all siliques and opened flowers.

The pots were then immersed upside down in the mixture of *Agrobacterium* infiltration medium as described above for 30 sec, and placed on their sides to allow draining into a 1' x 2' flat surface covered with plastic wrap. After 24 h, the plastic wrap was removed and pots are turned upright. The immersion procedure was repeated one week later, for a total of two immersions per pot. Seeds were then collected from each transformation pot and analyzed following the protocol described below.

Example V: Identification of *Arabidopsis* Primary Transformants

Seeds collected from the transformation pots were sterilized essentially as follows. Seeds were dispersed into in a solution containing 0.1% (v/v) Triton X-100 (Sigma) and sterile H_2O and washed by shaking the suspension for 20 min. The wash solution was then drained and replaced with fresh wash solution to wash the seeds for 20 min with shaking. After removal of the second wash solution, a solution containing 0.1% (v/v) Triton X-100 and 70% ethanol (Equistar) was added to the seeds and the suspension was shaken for 5 min. After removal of the ethanol/detergent solution, a solution containing 0.1% (v/v) Triton X-100 and 30% (v/v) bleach (Clorox) was added to the seeds, and the suspension was shaken for 10 min. After removal of the bleach/detergent solution, seeds were then washed five times in sterile distilled H_2O. The seeds were stored in the last wash water at 4° C for 2 days in the dark before being plated onto antibiotic selection medium (1 X Murashige and Skoog salts (pH adjusted to 5.7 with 1M KOH), 1 X Gamborg's B-5 vitamins, 0.9% phytagar (Life Technologies), and 50 mg/l kanamycin). Seeds were germinated under continuous illumination (50-75 $\mu E/m^2/sec$) at 22-23° C. After 7-10 days of growth under these conditions, kanamycin resistant primary transformants (T_1 generation) were visible and obtained. These seedlings were transferred first to fresh selection plates where the seedlings continued to grow for 3-5 more days, and then to soil (Pro-Mix BX potting medium).

Primary transformants were crossed and progeny seeds (T_2) collected; kanamycin resistant seedlings were selected and analyzed. The expression levels of the recombinant polynucleotides in the transformants varies from about a 5% expression level increase to a least a 100% expression level increase. Similar observations are made with respect to polypeptide level expression.

Example VI: Identification of *Arabidopsis* Plants with Transcription Factor Gene Knockouts

The screening of insertion mutagenized *Arabidopsis* collections for null mutants in a known target gene was essentially as described in Krysan et al (1999) Plant Cell 11:2283-2290. Briefly, gene-specific primers, nested by 5-250 base pairs to each other, were designed from the 5' and 3' regions of a known target gene. Similarly, nested sets of primers were also created specific to each of the T-DNA or

transposon ends (the "right" and "left" borders). All possible combinations of gene specific and T-DNA/transposon primers were used to detect by PCR an insertion event within or close to the target gene. The amplified DNA fragments were then sequenced which allows the precise determination of the T-DNA/transposon insertion point relative to the target gene. Insertion events within the coding or intervening sequence of the genes were deconvoluted from a pool comprising a plurality of insertion events to a single unique mutant plant for functional characterization. The method is described in more detail in Yu and Adam, US Application Serial No. 09/177,733 filed October 23, 1998.

Example VII: Identification of Modified Phenotypes in Overexpression or Gene Knockout Plants

Experiments were performed to identify those transformants or knockouts that exhibited modified biochemical characteristics. Among the biochemicals that were assayed were insoluble sugars, such as arabinose, fucose, galactose, mannose, rhamnose or xylose or the like; prenyl lipids, such as lutein, beta-carotene, xanthophyll-1, xanthophyll-2, chlorophylls A or B, or alpha-, delta- or gamma-tocopherol or the like; fatty acids, such as 16:0 (palmitic acid), 16:1 (palmitoleic acid), 18:0 (stearic acid), 18:1 (oleic acid), 18:2 (linoleic acid), 20:0 , 18:3 (linolenic acid), 20:1 (eicosenoic acid), 20:2, 22:1 (erucic acid) or the like; waxes, such as by altering the levels of C29, C31, or C33 alkanes; sterols, such as brassicasterol, campesterol, stigmasterol, sitosterol or stigmastanol or the like, glucosinolates, protein or oil levels.

Fatty acids were measured using two methods depending on whether the tissue was from leaves or seeds. For leaves, lipids were extracted and esterified with hot methanolic H_2SO_4 and partitioned into hexane from methanolic brine. For seed fatty acids, seeds were pulverized and extracted in methanol:heptane:toluene:2,2-dimethoxypropane:H_2SO_4 (39:34:20:5:2) for 90 minutes at 80°C. After cooling to room temperature the upper phase, containing the seed fatty acid esters, was subjected to GC analysis. Fatty acid esters from both seed and leaf tissues were analyzed with a Supelco SP-2330 column.

Glucosinolates were purified from seeds or leaves by first heating the tissue at 95°C for 10 minutes. Preheated ethanol:water (50:50) is and after heating at 95°C for a further 10 minutes, the extraction solvent is applied to a DEAE Sephadex column which had been previously equilibrated with 0.5 M pyridine acetate. Desulfoglucosinolates were eluted with 300 ul water and analyzed by reverse phase HPLC monitoring at 226 nm.

For wax alkanes, samples were extracted using an identical method as fatty acids and extracts were analyzed on a HP 5890 GC coupled with a 5973 MSD. Samples were chromatographically isolated on a J&W DB35 mass spectrometer (J&W Scientific).

To measure prenyl lipids levels, seeds or leaves were pulverized with 1 to 2% pyrogallol as an antioxidant. For seeds, extracted samples were filtered and a portion removed for tocopherol and carotenoid/chlorophyll analysis by HPLC. The remaining material was saponified for sterol determination. For leaves, an aliquot was removed and diluted with methanol and chlorophyll A, chlorophyll B, and total carotenoids measured by spectrophotometry by determining optical absorbance at 665.2 nm, 652.5 nm, and 470 nm. An aliquot was removed for tocopherol and carotenoid/chlorophyll composition by HPLC using a Waters uBondapak C18 column (4.6 mm x 150 mm). The remaining methanolic solution was saponified with 10% KOH at 80°C for one hour. The samples were cooled and diluted with a mixture of methanol and water. A solution of 2% methylene chloride in hexane was mixed in and the samples were centrifuged. The aqueous methanol phase was again re-extracted 2% methylene chloride in hexane and, after centrifugation, the two upper phases were combined and evaporated. 2% methylene chloride in hexane was added to the tubes and the samples were then extracted with one ml of water. The upper phase was removed, dried, and resuspended in 400 ul of 2% methylene chloride in hexane and analyzed by gas chromatography using a 50 m DB-5ms (0.25 mm ID, 0.25 um phase, J&W Scientific).

Insoluble sugar levels were measured by the method essentially described by Reiter et al., (1997) Plant Journal 12:335-345. This method analyzes the neutral sugar composition of cell wall polymers found in *Arabidopsis* leaves. Soluble sugars were

separated from sugar polymers by extracting leaves with hot 70% ethanol. The remaining residue containing the insoluble polysaccharides was then acid hydrolyzed with allose added as an internal standard. Sugar monomers generated by the hydrolysis were then reduced to the corresponding alditols by treatment with NaBH4, then were acetylated to generate the volatile alditol acetates which were then analyzed by GC-FID. Identity of the peaks was determined by comparing the retention times of known sugars converted to the corresponding alditol acetates with the retention times of peaks from wild-type plant extracts. Alditol acetates were analyzed on a Supelco SP-2330 capillary column (30 m x 250 um x 0.2 um) using a temperature program beginning at 180° C for 2 minutes followed by an increase to 220° C in 4 minutes. After holding at 220° C for 10 minutes, the oven temperature is increased to 240° C in 2 minutes and held at this temperature for 10 minutes and brought back to room temperature.

To identify plants with alterations in total seed oil or protein content, 150mg of seeds from T2 progeny plants were subjected to analysis by Near Infrared Reflectance Spectroscopy (NIRS) using a Foss NirSystems Model 6500 with a spinning cup transport system. NIRS is a non-destructive analytical method used to determine seed oil and protein composition. Infrared is the region of the electromagnetic spectrum located after the visible region in the direction of longer wavelengths. 'Near infrared' owns its name for being the infrared region near to the visible region of the electromagnetic spectrum. For practical purposes, near infrared comprises wavelengths between 800 and 2500 nm. NIRS is applied to organic compounds rich in O-H bonds (such as moisture, carbohydrates, and fats), C-H bonds (such as organic compounds and petroleum derivatives), and N-H bonds (such as proteins and amino acids). The NIRS analytical instruments operate by statistically correlating NIRS signals at several wavelengths with the characteristic or property intended to be measured. All biological substances contain thousands of C-H, O-H, and N-H bonds. Therefore, the exposure to near infrared radiation of a biological sample, such as a seed, results in a complex spectrum which contains qualitative and quantitative information about the physical and chemical composition of that sample.

The numerical value of a specific analyte in the sample, such as protein content or oil content, is mediated by a calibration approach known as chemometrics.

Chemometrics applies statistical methods such as multiple linear regression (MLR), partial least squares (PLS), and principle component analysis (PCA) to the spectral data and correlates them with a physical property or other factor, that property or factor is directly determined rather than the analyte concentration itself. The method first provides "wet chemistry" data of the samples required to develop the calibration.

Calibration for Arabidopsis seed oil composition was performed using accelerated solvent extraction using 1 g seed sample size and was validated against certified canola seed. A similar wet chemistry approach was performed for seed protein composition calibration.

Data obtained from NIRS analysis was analyzed statistically using a nearest-neighbor (N-N) analysis. The N-N analysis allows removal of within-block spatial variability in a fairly flexible fashion which does not require prior knowledge of the pattern of variability in the chamber. Ideally, all hybrids are grown under identical experimental conditions within a block (rep). In reality, even in many block designs, significant within-block variability exists. Nearest-neighbor procedures are based on assumption that environmental effect of a plot is closely related to that of its neighbors. Nearest-neighbor methods use information from adjacent plots to adjust for within-block heterogeneity and so provide more precise estimates of treatment means and differences. If there is within-plot heterogeneity on a spatial scale that is larger than a single plot and smaller than the entire block, then yields from adjacent plots will be positively correlated. Information from neighboring plots can be used to reduce or remove the unwanted effect of the spatial heterogeneity, and hence improve the estimate of the treatment effect. Data from neighboring plots can also be used to reduce the influence of competition between adjacent plots. The Papadakis N-N analysis can be used with designs to remove within-block variability that would not be removed with the standard split plot analysis (Papadakis, 1973, Inst. d'Amelior. Plantes Thessaloniki (Greece) Bull. Scientif., No. 23; Papadakis, 1984, Proc. Acad. Athens, 59, 326-342).

Experiments were performed to identify those transformants or knockouts that exhibited an improved pathogen tolerance. For such studies, the transformants were exposed to biotropic fungal pathogens, such as *Erysiphe orontii*, and necrotropic

fungal pathogens, such as *Fusarium oxysporum*. *Fusarium oxysporum* isolates cause vascular wilts and damping off of various annual vegetables, perennials and weeds (Mauch-Mani and Slusarenko (1994) Molecular Plant-Microbe Interactions 7: 378-383). For *Fusarium oxysporum* experiments, plants grown on Petri dishes were sprayed with a fresh spore suspension of *F. oxysporum*. The spore suspension was prepared as follows: A plug of fungal hyphae from a plate culture was placed on a fresh potato dextrose agar plate and allowed to spread for one week. 5 ml sterile water was then added to the plate, swirled, and pipetted into 50 ml Armstrong Fusarium medium. Spores were grown overnight in Fusarium medium and then sprayed onto plants using a Preval paint sprayer. Plant tissue was harvested and frozen in liquid nitrogen 48 hours post infection.

Erysiphe orontii is a causal agent of powdery mildew. For *Erysiphe orontii* experiments, plants were grown approximately 4 weeks in a greenhouse under 12 hour light (20°C, ~30% relative humidity (rh)). Individual leaves were infected with *E. orontii* spores from infected plants using a camel's hair brush, and the plants were transferred to a Percival growth chamber (20°C, 80% rh.). Plant tissue was harvested and frozen in liquid nitrogen 7 days post infection.

Botrytis cinerea is a necrotrophic pathogen. Botrytis cinerea was grown on potato dextrose agar in the light. A spore culture was made by spreading 10 ml of sterile water on the fungus plate, swirling and transferring spores to 10 ml of sterile water. The spore inoculum (approx. 105 spores/ml) was used to spray 10 day-old seedlings grown under sterile conditions on MS (minus sucrose) media. Symptoms were evaluated every day up to approximately 1 week.

Infection with bacterial pathogens Pseudomonas syringae pv maculicola (Psm) strain 4326 and pv maculicola strain 4326 was performed by hand inoculation at two doses. Two inoculation doses allows the differentiation between plants with enhanced susceptibility and plants with enhanced resistance to the pathogen. Plants were grown for 3 weeks in the greenhouse, then transferred to the growth chamber for the remainder of their growth. Psm ES4326 was hand inoculated with 1 ml syringe on 3 fully-expanded leaves per plant (4 1/2 wk old), using at least 9 plants per overexpressing line at two inoculation doses, OD=0.005 and OD=0.0005. Disease

scoring occurred at day 3 post-inoculation with pictures of the plants and leaves taken in parallel.

In some instances, expression patterns of the pathogen-induced genes (such as defense genes) was monitored by microarray experiments. cDNAs were generated by PCR and resuspended at a final concentration of ~ 100 ng/ul in 3X SSC or 150mM Na-phosphate (Eisen and Brown (1999) *Methods Enzymol.* 303:179-205). The cDNAs were spotted on microscope glass slides coated with polylysine. The prepared cDNAs were aliquoted into 384 well plates and spotted on the slides using an x-y-z gantry (OmniGrid) purchased from GeneMachines (Menlo Park, CA) outfitted with quill type pins purchased from Telechem International (Sunnyvale, CA). After spotting, the arrays were cured for a minimum of one week at room temperature, rehydrated and blocked following the protocol recommended by Eisen and Brown (1999; supra).

Sample total RNA (10 ug) samples were labeled using fluorescent Cy3 and Cy5 dyes. Labeled samples were resuspended in 4X SSC/0.03% SDS/4 ug salmon sperm DNA/2 ug tRNA/ 50mM Na-pyrophosphate, heated for 95°C for 2.5 minutes, spun down and placed on the array. The array was then covered with a glass coverslip and placed in a sealed chamber. The chamber was then kept in a water bath at 62°C overnight. The arrays were washed as described in Eisen and Brown (1999) and scanned on a General Scanning 3000 laser scanner. The resulting files are subsequently quantified using Imagene, a software purchased from BioDiscovery (Los Angeles, CA).

Experiments were performed to identify those transformants or knockouts that exhibited an improved environmental stress tolerance. For such studies, the transformants were exposed to a variety of environmental stresses. Plants were exposed to chilling stress (6 hour exposure to 4-8° C), heat stress (6 hour exposure to 32-37° C), high salt stress (6 hour exposure to 200 mM NaCl), drought stress (168 hours after removing water from trays), osmotic stress (6 hour exposure to 3 M mannitol), or nutrient limitation (nitrogen, phosphate, and potassium) (Nitrogen: all components of MS medium remained constant except N was reduced to 20 mg/l of NH_4NO_3, or Phosphate: All components of MS medium except KH_2PO_4, which was

replaced by K_2SO_4, Potassium: All components of MS medium except removal of KNO_3 and KH_2PO_4, which were replaced by NaH_4PO_4).

Experiments were performed to identify those transformants or knockouts that exhibited a modified structure and development characteristics. For such studies, the transformants were observed by eye to identify novel structural or developmental characteristics associated with the ectopic expression of the polynucleotides or polypeptides of the invention.

Experiments were performed to identify those transformants or knockouts that exhibited modified sugar-sensing. For such studies, seeds from transformants were germinated on media containing 5% glucose or 9.4% sucrose which normally partially restrict hypocotyl elongation. Plants with altered sugar sensing may have either longer or shorter hypocotyls than normal plants when grown on this media. Additionally, other plant traits may be varied such as root mass.

Flowering time was measured by the number of rosette leaves present when a visible inflorescence of approximately 3 cm is apparent Rosette and total leaf number on the progeny stem are tightly correlated with the timing of flowering (Koornneef et al (1991) *Mol. Gen. Genet* 229:57-66. The vernalization response was measured. For vernalization treatments, seeds were sown to MS agar plates, sealed with micropore tape, and placed in a 4°C cold room with low light levels for 6-8 weeks. The plates were then transferred to the growth rooms alongside plates containing freshly sown non-vernalized controls. Rosette leaves were counted when a visible inflorescence of approximately 3 cm was apparent.

Modified phenotypes observed for particular overexpressor or knockout plants are provided in Table 4. For a particular overexpressor that shows a less beneficial characteristic, it may be more useful to select a plant with a decreased expression of the particular transcription factor. For a particular knockout that shows a less beneficial characteristic, it may be more useful to select a plant with an increased expression of the particular transcription factor.

The sequences of the Sequence Listing or those in Tables 4 , 5 or those disclosed here can be used to prepare transgenic plants and plants with altered traits. The specific transgenic plants listed below are produced from the sequences of the Sequence Listing, as noted. Table 4 provides exemplary polynucleotide and polypeptide sequences of the invention. Table 4 includes, from left to right for each sequence: the first column shows the polynucleotide SEQ ID NO; the second column shows the Mendel Gene ID No., GID; the third column shows the trait(s) resulting from the knock out or overexpression of the polynucleotide in the transgenic plant; the fourth column shows the category of the trait; the fifth column shows the transcription factor family to which the polynucleotide belongs; the sixth column ("Comment"), includes specific effects and utilities conferred by the polynucleotide of the first column; the seventh column shows the SEQ ID NO of the polypeptide encoded by the polynucleotide; and the eighth column shows the amino acid residue positions of the conserved domain in amino acid (AA) co-ordinates.

Seed of plants overexpressing sequences G265 (SEQ ID NOs:871 and 872), G715 (SEQ ID NOs:925 and 926), G1471 (SEQ ID NOs:311 and 312), G1793 (SEQ ID NOs:365 and 366), G1838 (SEQ ID NOs:381 and 382), G1902 (SEQ ID NOs:405 and 406), G286 (SEQ ID NOs:877 and 878), G2138 (SEQ ID NOs:865 and 866) and G2830 (SEQ ID NOs:875 and 876) was subjected to NIR analysis and a significant increase in seed oil content compared with seed from control plants was identified.

G192: G192 (SEQ ID NO: 859) was expressed in all plant tissues and under all conditions examined. Its expression was slightly induced upon infection by Fusarium. G192 was analyzed using transgenic plants in which this gene was expressed under the control of the 35S promoter. G192 overexpressors were late flowering under 12 hour light and had more leaves than control plants. This phenotype was manifested in the three T2 lines analyzed. Results of one experiment suggest that G192 overexpressor was more susceptible to infection with a moderate dose of the fungal pathogen Erysiphe orontii. The decrease in seed oil observed for one line was replicated in an independent experiment. G192 overexpression delayed flowering. A wide variety of applications exist for systems that either lengthen or shorten the time to flowering, or for systems of inducible flowering time control. In particular, in species where the vegetative parts of the plants constitute the crop and

the reproductive tissues are discarded, it will be advantageous to delay or prevent flowering. Extending vegetative development can bring about large increases in yields. G192 can be used to manipulate the defense response in order to generate pathogen-resistant plants. G192 can be used to manipulate seed oil content, which can be of nutritional value.

Closely Related Genes from Other Species

G192 had some similarity within the conserved WRKY domain to non-Arabidopsis plant proteins.

G1946: G1946 (SEQ ID NO: 801) was studied using transgenic plants in which the gene was expressed under the control of the 35S promoter. Overexpression of G1946 resulted in accelerated flowering, with 35S::G1946 transformants producing flower buds up to a week earlier than wild-type controls (24-hour light conditions). These effects were seen in 12/20 primary transformants and in two independent plantings of each of the three T2 lines. Unlike many early flowering Arabidopsis transgenic lines, which are dwarfed, 35S::G1946 transformants often reached full-size at maturity, and produced large quantities of seeds, although the plants were slightly pale in coloration and had slightly flat leaves compared to wild-type. In addition, 35S::G1946 plants showed an altered response to phosphate deprivation. Seedlings of G1946 overexpressor plants showed more secondary root growth on phosphate-free media, when compared to wild-type control. In a repeat experiment, all three lines showed the phenotype. Overexpression of G1946 in Arabidopsis also resulted in an increase in seed glucosinolate M39501 in T2 lines 1and 3. An increase in seed oil and a decrease in seed protein was also observed in these two lines. G1946 was ubiquitously expressed, and does not appear to be significantly induced or repressed by any of the biotic and abiotic stress conditions tested at this time, with the exception of cold, which repressed G1946 expression. G1946 can be used to modify flowering time, as well as to improve the plant's performance in conditions of limited phosphate, and to alter seed oil, protein, and glucosinolate composition.

Closely Related Genes from Other Species

A comparison of the amino acid sequence of G1946 with sequences available from GenBank showed strong similarity with plant HSFs of several species (Lycopersicon peruvianum, Medicago truncatula, Lycopersicon esculentum, Glycine max, Solanum tuberosum, Oryza sativa and Hordeum vulgare subsp. vulgare).

G375: The sequence of G375 (SEQ ID NO:239) was experimentally determined and G375 was analyzed using transgenic plants in which G375 was expressed under the control of the 35S promoter. Overexpression of G375 produced marked effects on leaf development. At early stages of growth, 35S::G375 seedlings developed narrow, upward pointing leaves with long petioles (possibly indicating a disruption in circadian-clock controlled processes or nyctinastic movements). Additionally, some seedlings were noted to have elongated hypocotyls, and some were rather small compared to wild-type controls. Comparable phenotypes were obtained by overexpression of an AP2 family gene, G2113 (SEQ ID NO: 85). Following the switch to flowering, 35S::G375 plants showed reduced fertility, which possibly arose from a failure of stamens to fully elongate. One of the three T2 lines, (#41) was later flowering than wild-type controls, and also developed large numbers of small secondary rosette leaves in the axils of the primary rosette. Although these effects were not noted in the other two lines, the phenotypes obtained in line 41 were somewhat similar to those produced by overexpression of another Z-dof gene, G736 (SEQ ID NO: 211). G375 was expressed in all tissues, although at different levels. It was expressed at low levels in the root and germinating seed, and expressed at high levels in the embryo. The effects of G375 on leaf architecture are of potential interest to the ornamental horticulture industry.

Closely Related Genes from Other Species

G375 showed some homology to non-Arabidopsis plant proteins within the conserved Dof domain.

G1255: The sequence of G1255 (SEQ ID NO: 273) was experimentally determined and G1255 was analyzed using transgenic plants in which G1255 was expressed under the control of the 35S promoter. Plants overexpressing G1255 had

alterations in leaf architecture, a reduction in apical dominance, an increase in seed size, and showed more disease symptoms following inoculation with a low dose of the fungal pathogen Botrytis cinerea. G1255 was constitutively expressed and not significantly induced by any conditions tested. On the basis of the phenotypes produced by overexpression of G1255, G1255 can be used to manipulate the plant's defense response to produce pathogen resistance, alter plant architecture, or alter seed size.

Closely Related Genes from Other Species

G1255 showed strong homology to a putative rice zing finger protein represented by sequence AC087181_3. Sequence identity between these two protein extended beyond the conserved domain, and therefore, these genes can be orthologs.

G865: The complete cDNA sequence of G865 (SEQ ID NO: 557) was determined. G865 was ubiquitously expressed in Arabidopsis tissues. G865 was analyzed using transgenic plants in which G865 was expressed under the control of the 35S promoter. Plants overexpressing G865 were early flowering, with numerous secondary inflorescence meristems giving them a bushy appearance. G865 overexpressors were more susceptible to infection with a moderate dose of the fungal pathogens Erysiphe orontii and Botrytis cinerea. In addition, seeds from G865 overexpressing plants showed a trend of increased protein and reduced oil content, although the observed changes were not beyond the criteria used for judging significance except in one line. G865 can be used to control flowering time. G865 can be used to manipulate the defense response in order to generate pathogen-resistant plants. G865 can be used to alter seed oil and protein content of a plant.

Closely Related Genes from Other Species

G865 and other non-Arabidopsis AP2/EREBP proteins were similar within the conserved AP2 domain.

G2509: G2509 (SEQ ID NO: 23) was studied using transgenic plants in which the gene was expressed under the control of the 35S promoter. Overexpression of G2509 caused multiple alterations in plant growth and development, most notably, altered branching patterns, and a reduction in apical dominance, giving the plants a

shorter, more bushy stature than wild type. Twenty 35S::G2509 primary transformants were examined; at early stages of rosette development, these plants displayed a wild-type phenotype. However, at the switch to flowering, almost all T1 lines showed a marked loss of apical dominance and large numbers of secondary shoots developed from axils of primary rosette leaves. In the most extreme cases, the shoots had very short internodes, giving the inflorescence a very bushy appearance. Such shoots were often very thin and flowers were relatively small and poorly fertile. At later stages, many plants appeared very small and had a low seed yield compared to wild type. In addition to the effects on branching, a substantial number of 35S::G2509 primary transformants also flowered early and had buds visible several days prior to wild type. Similar effects on inflorescence development were noted in each of three T2 populations examined. The branching and plant architecture phenotypes observed in 35S::G2509 lines resemble phenotypes observed for three other AP2/EREBP genes: G865 (SEQ ID NO: 557), G1411 (SEQ ID NO: 3), and G1794 (SEQ ID NO: 13). G2509, G865, and G1411 form a small clade within the large AP2/EREBP family, and G1794, although not belonging to the clade, is one of the AP2/EREBP genes closest to it in the phylogenetic tree. It is thus likely that all these genes share a related function, such as affecting hormone balance. Overexpression of G2509 in Arabidopsis resulted in an increase in alpha-tocopherol in seeds in T2 lines 5 and 11. G2509 was ubiquitously expressed in Arabidopsis plant tissue. G2509 expression levels were altered by a variety of environmental or physiological conditions. G2509 can be used to manipulate plant architecture and development. G2509 can be used to alter tocopherol composition. Tocopherols have anti-oxidant and vitamin E activity. G2509 can be useful in altering flowering time. A wide variety of applications exist for systems that either lengthen or shorten the time to flowering.

Closely Related Genes from Other Species

G2509 showed some sequence similarity with known genes from other plant species within the conserved AP2/EREBP domain.

G2347: G2347 (SEQ ID NO: 1119) was analyzed using transgenic plants in which G2347 was expressed under the control of the 35S promoter. Overexpression of G2347 markedly reduced the time to flowering in Arabidopsis. This phenotype

was apparent in the majority of primary transformants and in all plants from two out of the three T2 lines examined. Under continuous light conditions, 35S::G2347 plants formed flower buds up a week earlier than wild type. Many of the plants were rather small and spindly compared to controls. To demonstrate that overexpression of G2347 could induce flowering under less inductive photoperiods, two T2 lines were re-grown in 12 hour conditions; again, all plants from both lines bolted early, with some initiating flower buds up to two weeks sooner than wild-type. As determined by RT-PCR, G2347 was highly expressed in rosette leaves and flowers, and to much lower levels in embryos and siliques. No expression of G2347 was detected in the other tissues tested. G2347 expression was repressed by cold, and by auxin treatments and by infection by Erysiphe. G2347 is also highly similar to the Arabidopsis protein G2010 (SEQ ID NO: 1121). The level of homology between these two proteins suggested they could have similar, overlapping, or redundant functions in Arabidopsis. In support of this hypothesis, overexpression of both G2010 and G2347 resulted in early flowering phenotypes in transgenic plants.

Closely Related Genes from Other Species

The closest relative to G2347 is the Antirrhinum protein, SBP2 (CAA63061). The similarity between these two proteins is extensive enough to suggest they might have similar functions in a plant.

G988: G988 (SEQ ID NO: 43) was analyzed using transgenic plants in which G988 was expressed under the control of the 35S promoter. Plants overexpressing G988 had multiple morphological phenotypes. The transgenic plants were generally smaller than wild-type plants, had altered leaf, inflorescence and flower development, altered plant architecture, and altered vasculature. In one transgenic line overexpressing G988 (line 23), an increase in the seed glucosinolate M39489 was observed. The phenotype of plants overexpressing G988 was wild-type in all other assays performed. In wild-type plants, G988 was expressed primarily in flower and silique tissue, but was also present at detectable levels in all other tissues tested. Expression of G988 was induced in response to heat treatment, and repressed in response to infection with Erysiphe. Based on the observed morphological phenotypes of the transgenic plants, G988 can be used to create plants with larger flowers. This can have value in the ornamental horticulture industry. The reduction

in the formation of lateral branches suggests that G988 can have utility on the forestry industry. The Arabidopsis plants overexpressing G988 also had reduced fertility. This can be a desirable trait in some instances, as it can be exploited to prevent or minimize the escape of GMO (genetically modified organism) pollen into the environment.

Closely Related Genes from Other Species

The amino acid sequence for the Capsella rubella hypothetical protein represented by GenBank accession number CRU303349 was significantly identical to G988 outside of the SCR conserved domains. The Capsella rubella hypothetical protein is 90% identical to G988 over a stretch of roughly 450 amino acids. Therefore, it is likely that the Capsella rubella gene is an ortholog of G988.

G2346: G2346 (SEQ ID NO: 459) was analyzed using transgenic plants in which the gene was expressed under the control of the 35S promoter. 35S::G2346 seedlings from all three T2 populations had slightly larger cotyledons and appeared somewhat more advanced than controls. This indicated that the seedlings developed more rapidly that the control plants. At later stages, however, G2346 overexpressing plants showed no consistent differences from control plants. The phenotype of these transgenic plants was wild-type in all other assays performed. According to RT-PCR analysis, G2346 is expressed ubiquitously.

Closely Related Genes from Other Species

G2346 shows some sequence similarity with known genes from other plant species within the conserved SBP domain.

G1354: The complete sequence of G1354 (SEQ ID NO: 285) was determined. G1354 was analyzed using transgenic plants in which G1354 was expressed under the control of the 35S promoter. Overexpression of G1354 produced highly deleterious effects on growth and development. Only three 35S::G1354 T1 plants were obtained; all were extremely tiny and slow developing. After three weeks of growth, each of the plants comprised a completely disorganized mass of leaves and root that had no clear axis of growth. Since these individuals would not have survived transplantation to soil, they were harvested for RT-PCR analysis; all three plants showed moderate

levels of G1354 overexpression compared to whole wild-type seedlings of an equivalent size. Only a very small number of transformants were obtained from two selection attempts on separate batches of T0 seed. Usually between 15 and 120 transformants are obtained from each aliquot of 300 mg T0 seed from wild-type plants. The low transformation frequency obtained in this experiment suggests that high levels of G1354 overexpression might have completely lethal effects and prevent transformed seeds from germinating. As determined by RT-PCR, G1354 was uniformly expressed in all tissues and under all conditions tested in RT-PCR. However, the gene was repressed in leaf tissue in response to Erysiphe infection.

Closely Related Genes from Other Species

G1354 is closely related to a NAM protein encoded by polynucleotide from rice (AC005310). Similarity between G1354 and this rice protein extends beyond the signature motif of the family to a level that would suggest the genes are orthologs.

G1063: G1063 (SEQ ID NO: 119) is a member of a clade of highly related HLH/MYC proteins that also includes G779 (SEQ ID NO: 113), G1499 (SEQ ID NO: 7), G2143 (SEQ ID NO: 129), and G2557 (SEQ ID NO: 133). All of these genes caused similar pleiotropic phenotypic effects when overexpressed, the most striking of which was the production of ectopic carpelloid tissue. These genes can be considered key regulators of carpel development. A spectrum of developmental alterations was observed amongst 35S::G1063 primary transformants and the majority were markedly small, dark green, and had narrow curled leaves. The most severely affected individuals were completely sterile and formed highly abnormal inflorescences; shoots often terminated in pin-like structures, and flowers were replaced by filamentous carpelloid structures. In other cases, flowers showed internode elongation between floral whorls, with a central carpel protruding on a pedicel-like organ. Additionally, lateral branches sometimes failed to develop and tiny patches of carpelloid tissue formed at axillary nodes of the inflorescence. In lines with an intermediate phenotype, flowers contained defined whorls of organs, but sepals were converted to carpelloid structures or displayed patches of carpelloid tissue. In contrast, lines with a weak phenotype developed relatively normal flowers and produced a reasonable quantity of seed. Such plants were still distinctly smaller than wild-type controls. Since the strongest 35S::G1063 lines were sterile, three lines

with a relatively weak phenotype, that had produced sufficient seed for biochemical and physiological analysis, were selected for further study. Two of the T2 populations (T2-28,37) were clearly small, darker green and possessed narrow leaves compared to wild type. Plants from one of these populations (T2-28) also produced occasional branches with abnormal flowers like those seen in the T1. The final T2 population (T2-30) displayed a very mild phenotype. Overexpression of G1063 in Arabidopsis resulted in a decrease in seed oil content in T2 lines 28 and 37. No altered phenotypes were detected in any of the physiological assays, except that the plants were noted to be somewhat small and produce anthocyanin when grown in Petri plates. G1063 was expressed at low to moderate levels in roots, flowers, rosette leaves, embryos, and germinating seeds, but was not detected in shoots or siliques. It was induced by auxin. G1063 can be used to manipulate flower form and structure or plant fertility. One application for manipulation of flower structure can be in the production of saffron, which is derived from the stigmas of Crocus sativus. G1063 has utility in manipulating seed oil and protein content.

Closely Related Genes from Other Species

G1063 protein shared extensive homology in the basic helix loop helix region with a protein sequence encoded by Glycine max cDNA clone (AW832545) as well as a tomato root, plants pre-anthesis Lycopersicon sculentum cDNA (BE451174).

G2143: G2143 (SEQ ID NO: 129) is a member of a clade of highly related HLH/MYC proteins that also includes G779 (SEQ ID NO: 113), G1063 (SEQ ID NO: 119), G1499 (SEQ ID NO: 7), and G2557 (SEQ ID NO: 133). All of these genes caused similar pleiotropic phenotypic effects when overexpressed, the most striking of which was the production of ectopic carpelloid tissue. These genes can be considered key regulators of carpel development. Twelve out of twenty 35S::G2143 T1 lines showed a very severe phenotype; these plants were markedly small and had narrow, curled, dark-green leaves. Such individuals were completely sterile and formed highly abnormal inflorescences; shoots often terminated in pin-like structures, and flowers were replaced by filamentous carpelloid structures, or a fused mass of carpelloid tissue. Furthermore, lateral branches usually failed to develop, and tiny patches of stigmatic tissue often formed at axillary nodes of the inflorescence. Strongly affected plants displayed the highest levels of transgene expression

(determined by RT-PCR). The remaining T1 lines showed lower levels of G2143 overexpression; these plants were still distinctly smaller than wild type, but had relatively normal inflorescences and produced seed. Since the strongest 35S::G2143 lines were sterile, three lines with a relatively weak phenotype, that had produced sufficient seed for biochemical analysis, were selected for further study. T2-11 plants displayed a very mild phenotype and had somewhat small, narrow, dark green leaves. The other two T2 populations, however, appeared wild-type, suggesting that transgene activity might have been reduced between the generations. Reduced seedling vigor was noted in the physiological assays. G2143 expression was detected at low levels in flowers and siliques, and at higher levels in germinating seed. G2143 can be used to manipulate flower form and structure or plant fertility. One application for manipulation of flower structure can be in the production of saffron, which is derived from the stigmas of Crocus sativus.

Closely Related Genes from Other Species

G2143 protein shared extensive homology in the basic helix loop helix region with a protein encoded by Glycine max cDNA clones (AW832545, BG726819 and BG154493) and a Lycopersicon esculentum cDNA clone (BE451174). There was lower homology outside of the region.

G2557: G2557 (SEQ ID NO: 133) is a member of a clade of highly related HLH/MYC proteins that also includes G779 (SEQ ID NO: 113), G1063 (SEQ ID NO: 119), G1499 (SEQ ID NO: 7), and G2143 (SEQ ID NO: 129). All of these genes caused similar pleiotropic phenotypic effects when overexpressed, the most striking of which was the production of ectopic carpelloid tissue. These genes can be considered key regulators of carpel development. The flowers of 35S::G2557 primary transformants displayed patches of stigmatic papillae on the sepals, and often had rather narrow petals and poorly developed stamens. Additionally, carpels were also occasionally held outside of the flower at the end of an elongated pedicel like structure. As a result of such defects, 35S::G2557 plants often showed very poor fertility and formed small wrinkled siliques. In addition to such floral abnormalities, the majority of primary transformants were also small and darker green in coloration than wild type. Approximately one third of the T1 plants were extremely tiny and completely sterile. Three T1 lines (#7,9,12), that had produced some seeds, and

showed a relatively weak phenotype, were chosen for further study. All three of the T2 populations from these lines contained plants that were distinctly small, had abnormal flowers, and were poorly fertile compared to controls. Stigmatic tissue was not noted on the sepals of plants from these three T2 lines. Another line (#4) that had shown a moderately strong phenotype in the T1 was sown for only morphological analysis in the T2 generation. T2-4 plants were small, dark green, and produced abnormal flowers with ectopic stigmatic tissue on the sepals, as had been seen in the parental plant. G2557 expression was detected at low to moderate levels in all tissues tested except shoots. It was induced by cold, heat, and salt, and repressed by pathogen infection. G1063 can be used to manipulate flower form and structure or plant fertility. One application for manipulation of flower structure can be in the production of saffron, which is derived from the stigmas of Crocus sativus.

Closely Related Genes from Other Species

G2557 protein shows extensive sequence similarity in the region of basic helix loop helix with a protein encoded by Glycine max cDNA clone (BE347811).

G2430: The complete sequence of G2430 (SEQ ID NO: 697) was determined. G2430 is a member of the response regulator class of GARP proteins (ARR genes), although one of the two conserved aspartate residues characteristic of response regulators is not present. The second aspartate, the putative phosphorylated site, is retained so G2430 can have response regulator function. G2430 is specifically expressed in embryo and silique tissue. In morphological analyses, plants overexpressing G2430 showed more rapid growth than control plants at early stages, and in two of three lines examined produced large, flat leaves. Early flowering was observed for some lines, but this effect was inconsistent between plantings. G2430 can regulate plant growth. Overexpression of G2430 in Arabidopsis also resulted in seedlings that are slightly more tolerant to heat in a germination assay. Seedlings from G2430 overexpressing transgenic plants were slightly greener than the control seedlings under high temperature conditions. In a repeat experiment on individual lines, G2430 line 15 showed the strongest heat tolerant phenotype. G2430 can be useful to promote faster development and reproduction in plants.

Closely Related Genes from Other Species

G2430 had some similarity within of the conserved GARP and response-regulator domains to non-Arabidopsis proteins.

G1478: The sequence of G1478 (SEQ ID NO: 831) was determined and G1478 was analyzed using transgenic plants in which G1478 was expressed under the control of the 35S promoter. Plants overexpressing G1478 had a general delay in progression through the life cycle, in particular a delay in flowering time. G1478 is expressed at higher levels in flowers, rosettes and embryos but otherwise expression is constitutive. Based on the phenotypes produced through G1478 overexpression, G1478 can be used to manipulate the rate at which plants grow, and flowering time.

Closely Related Genes from Other Species

G1478 shows some homology to non-Arabidopsis proteins within the conserved domain.

G681: G681 (SEQ ID NO: 579) was analyzed using transgenic plants in which the gene was expressed under the control of the 35S promoter. Approximately half of the 35S::G681 primary transformants were markedly small and formed narrow leaves compared to controls. These plants often produced thin inflorescence stems, had rather poorly formed flowers with low pollen production, and set few seeds. Three T1 lines with relatively weak phenotypes, which had produced reasonable quantities of seed, were selected for further study. Plants from one of the T2 populations were noted to be slightly small, but otherwise the T2 lines displayed no consistent differences in morphology from controls. In leaves of two of the T2 lines, overexpression of G681 resulted in an increase in the percentage of the glucosinolate M39480. According to RT-PCR analysis, G681 expression was detected at very low levels in flower and rosette leaf tissues. G681 was induced by drought stress. G681 can be used to alter glucosinolate composition in plants. Increases or decreases in specific glucosinolates or total glucosinolate content are desirable depending upon the particular application. For example: (1) Glucosinolates are undesirable components of the oilseeds used in animal feed, since they produce toxic effects. Low-glucosinolate varieties of canola have been developed to combat this problem. (2) Some glucosinolates have anti-cancer activity; thus, increasing the levels or

composition of these compounds might be of interest from a nutraceutical standpoint. (3) Glucosinolates form part of a plants natural defense against insects. Modification of glucosinolate composition or quantity could therefore afford increased protection from predators. Furthermore, in edible crops, tissue specific promoters can be used to ensure that these compounds accumulate specifically in tissues, such as the epidermis, which are not taken for consumption.

Closely Related Genes from Other Species

G681 shows some sequence similarity with known genes from other plant species within the conserved Myb domain.

G878: G878 (SEQ ID NO: 611) was studied using transgenic plants in which the gene was expressed under the control of the 35S promoter. Analysis of primary transformants revealed that overexpression of G878 delays the onset of flowering in Arabidopsis. 11/20 of the 35S::G878 T1 plants flowered approximately one week later than wild type under continuous light conditions. These plants were also darker green, had shorter stems, and senesced later than controls. G878 was ubiquitously expressed. G878 can be used to modify flowering time and senescence, and a wide variety of applications exist for systems that either lengthen or shorten the time to flowering.

Closely Related Genes from Other Species

G878 was highly related to other WRKY proteins from a variety of plant species, such as the Nicotiana tabacum DNA-binding protein 2 (WRKY2) (AF096299), and a Cucumis sativus SPF1-like DNA-binding protein (L44134).

G374: G374 (SEQ ID NO: 47) was expressed at low levels throughout the plant and was induced by salicylic acid. G374 was investigated using lines carrying a T-DNA insertion in this gene. The T-DNA insertion was approximately three quarters of the way into the protein coding sequence and should result in a null mutation. Homozygosity for a T-DNA insertion within G374 caused lethality at early stages of embryo development. In an initial screen for G374 knockouts, heterozygous plants were identified. Seed from those individuals was sown to soil and eleven plants were PCR-screened to identify homozygotes. No homozygotes were obtained;

6 of the progeny were heterozygous whilst the other 5 were wild type. This raised the prospect that homozygosity for the G374 insertion was lethal. To examine this possibility further, heterozygous KO.G374 plants were re-grown. These individuals looked wild type, but their siliques were examined for seed abnormalities. When green siliques were dissected, around 25% of developing seeds were white or aborted. Embryos from these siliques were cleared using Hoyers solution, and examined under the microscope. It was apparent that embryos from the white seeds had arrested at early (globular or heart) stages of development, whilst embryos from the normal seeds were fully developed. Such arrested or aborted seeds most likely represented homozygotes for the G374 insertion. To support this conclusion, seed was collected from heterozygous plants and sown to kanamycin plates (the T-DNA insertion carried the NPT marker gene). Of the seedlings that germinated, 160 were kanamycin resistant and 107 were kanamycin sensitive. These data more closely fitted a 2:1 (chi-sq., 1df, = 5.5, 0.05>P>0.01) than a 3:1 (chi-sq., 1df, = 32, P<0.001) ratio. Such a segregation ratio suggested that a homozygous class of kanamycin resistant seedlings was absent from the progeny of KO.G374 plant. G374 can be a herbicide target.

Closely Related Genes from Other Species

Similar sequences to G374 are present in tomato and Medicago truncatula, and these sequences can be orthologs.

Example VIII: Identification of Homologous Sequences

Homologous sequences from *Arabidopsis* and plant species other than *Arabidopsis* were identified using database sequence search tools, such as the Basic Local Alignment Search Tool (BLAST) (Altschul et al. (1990) J. Mol. Biol. 215:403-410; and Altschul et al. (1997) Nucl. Acid Res. 25: 3389-3402). The tblastx sequence analysis programs were employed using the BLOSUM-62 scoring matrix (Henikoff, S. and Henikoff, J. G. (1992) Proc. Natl. Acad. Sci. USA 89: 10915-10919).

Identified non-Arabidopsis sequences homologous to the *Arabidopsis* sequences are provided in Table 5. The percent sequence identity among these sequences can be as low as 47%, or even lower sequence identity. The entire NCBI GenBank database was filtered for sequences from all plants except *Arabidopsis thaliana* by selecting all entries in the NCBI GenBank database associated with NCBI

taxonomic ID 33090 (Viridiplantae; all plants) and excluding entries associated with taxonomic ID 3701 (*Arabidopsis thaliana*). These sequences are compared to sequences representing genes of SEQ IDs NOs:2 - 2N, where N = 2-561, using the Washington University TBLASTX algorithm (version 2.0a19MP) at the default settings using gapped alignments with the filter "off". For each gene of SEQ IDs NOs:2 - 2N, where N = 2-561, individual comparisons were ordered by probability score (P-value), where the score reflects the probability that a particular alignment occurred by chance. For example, a score of 3.6e-40 is 3.6×10^{-40}. In addition to P-values, comparisons were also scored by percentage identity. Percentage identity reflects the degree to which two segments of DNA or protein are identical over a particular length. Examples of sequences so identified are presented in Table 5. Homologous or orthologous sequences are readily identified and available in GenBank by Accession number (Table 5; Test sequence ID). The identified homologous polynucleotide and polypeptide sequences and homologues of the *Arabidopsis* polynucleotides and polypeptides may be orthologs of the *Arabidopsis* polynucleotides and polypeptides (TBD: to be determined).

Example IX Introduction of polynucleotides into dicotyledonous plants

SEQ ID NOs:1-(2N - 1), wherein N = 2-561, paralogous, orthologous, and homologous sequences recombined into pMEN20 or pMEN65 expression vectors are transformed into a plant for the purpose of modifying plant traits. The cloning vector may be introduced into a variety of cereal plants by means well-known in the art such as, for example, direct DNA transfer or *Agrobacterium tumefaciens*-mediated transformation. It is now routine to produce transgenic plants using most dicot plants (see Weissbach and Weissbach, (1989) *supra;* Gelvin et al., (1990) *supra*; Herrera-Estrella et al. (1983) *supra*; Bevan (1984) *supra*; and Klee (1985) *supra*). Methods for analysis of traits are routine in the art and examples are disclosed above.

Example X Transformation of Cereal Plants with an Expression Vector

Cereal plants such as corn, wheat, rice, sorghum or barley, may also be transformed with the present polynucleotide sequences in pMEN20 or pMEN65 expression vectors for the purpose of modifying plant traits. For example, pMEN020 may be modified to replace the NptII coding region with the BAR gene of *Streptomyces hygroscopicus* that confers resistance to phosphinothricin. The KpnI

and BglII sites of the Bar gene are removed by site-directed mutagenesis with silent codon changes.

The cloning vector may be introduced into a variety of cereal plants by means well-known in the art such as, for example, direct DNA transfer or *Agrobacterium tumefaciens*-mediated transformation. It is now routine to produce transgenic plants of most cereal crops (Vasil, I., Plant Molec. Biol. 25: 925-937 (1994)) such as corn, wheat, rice, sorghum (Cassas, A. et al., Proc. Natl. Acad Sci USA 90: 11212-11216 (1993) and barley (Wan, Y. and Lemeaux, P. Plant Physiol. 104:37-48 (1994). DNA transfer methods such as the microprojectile can be used for corn (Fromm. et al. Bio/Technology 8: 833-839 (1990); Gordon-Kamm et al. Plant Cell 2: 603-618 (1990); Ishida, Y., Nature Biotechnology 14:745-750 (1990)), wheat (Vasil, et al. Bio/Technology 10:667-674 (1992) ; Vasil et al., Bio/Technology 11:1553-1558 (1993); Weeks et al., Plant Physiol. 102:1077-1084 (1993)), rice (Christou Bio/Technology 9:957-962 (1991); Hiei et al. Plant J. 6:271-282 (1994); Aldemita and Hodges, Planta 199:612-617; Hiei et al., Plant Mol Biol. 35:205-18 (1997)). For most cereal plants, embryogenic cells derived from immature scutellum tissues are the preferred cellular targets for transformation (Hiei et al., Plant Mol Biol. 35:205-18 (1997); Vasil, Plant Molec. Biol. 25: 925-937 (1994)).

Vectors according to the present invention may be transformed into corn embryogenic cells derived from immature scutellar tissue by using microprojectile bombardment, with the A188XB73 genotype as the preferred genotype (Fromm, et al., Bio/Technology 8: 833-839 (1990); Gordon-Kamm et al., Plant Cell 2: 603-618 (1990)). After microprojectile bombardment the tissues are selected on phosphinothricin to identify the transgenic embryogenic cells (Gordon-Kamm et al., Plant Cell 2: 603-618 (1990)). Transgenic plants are regenerated by standard corn regeneration techniques (Fromm, et al., Bio/Technology 8: 833-839 (1990); Gordon-Kamm et al., Plant Cell 2: 603-618 (1990)).

The plasmids prepared as described above can also be used to produce transgenic wheat and rice plants (Christou, Bio/Technology 9:957-962 (1991); Hiei et al., Plant J. 6:271-282 (1994); Aldemita and Hodges, Planta 199:612-617 (1996); Hiei et al., Plant Mol Biol. 35:205-18 (1997)) that coordinately express genes of

interest by following standard transformation protocols known to those skilled in the art for rice and wheat Vasil, et al. Bio/Technology 10:667-674 (1992) ; Vasil et al., Bio/Technology 11:1553-1558 (1993); Weeks et al., Plant Physiol. 102:1077-1084 (1993)), where the bar gene is used as the selectable marker.

All references, publications, patent documents, web pages, and other documents cited or mentioned herein are hereby incorporated by reference in their entirety for all purposes. Although the invention has been described with reference to specific embodiments and examples, it should be understood that one of ordinary skill can make various modifications without departing from the spirit of the invention. The scope of the invention is not limited to the specific embodiments and examples provided.

We claim:

1. A transgenic plant comprising a recombinant polynucleotide having a nucleotide sequence selected from the group consisting of:
(a) a nucleotide sequence encoding a polypeptide comprising a sequence selected from those of SEQ ID NOs: 860, 802, 240, 274, 558, 24, 1120, 44, 460, 286, 120, 130, 134, 698, 832, 580, 612, and 48, or a complementary nucleotide sequence thereof;
(b) a nucleotide sequence of SEQ ID NOs: 859, 801, 239, 273, 557, 23, 1119, 43, 459, 285, 119, 129, 133, 697, 831, 579, 611, 47, or a complementary nucleotide sequence thereof; and
(c) a nucleotide sequence that hybridizes under stringent conditions to a nucleotide sequence of one or more polynucleotides of: (a) or (b).

2. The transgenic plant of claim 1 wherein the transgenic plant possesses an altered trait as compared to another plant, or the transgenic plant exhibits an altered phenotype as compared to another plant, or the transgenic plant expresses an altered level of one or more genes associated with a plant trait as compared to another plant, wherein the other plant does not comprise the recombinant polynucleotide.

3. The transgenic plant of claim 1 wherein the plant possesses an altered trait as compared to another plant wherein the trait is an alteration in one or more physical characteristics selected from the group consisting of: the number of trichomes, fruit and seed size and number, yield of stems, leaves, inflorescences, or roots, stability of seeds during storage, susceptibility of the seed to shattering, root hair length and quantity, internode distances, or the quality of seed coat.

4. The transgenic plant of claim 1 wherein the plant possesses an altered trait as compared to another plant wherein the trait is an alteration in a plant growth characteristic selected from the group consisting of: growth rate, germination rate of seeds, vigor of plants and seedlings, leaf and flower senescence, male sterility, apomixis, flowering time, flower abscission, rate of nitrogen uptake, osmotic sensitivity to soluble sugar concentrations, biomass or transpiration characteristics,

apical dominance, branching patterns, number of organs, organ identity, and organ shape or size.

5. The transgenic plant of claim 1 wherein the plant possesses an altered trait as compared to another plant wherein the trait is an alteration in one or more characteristics selected from the group consisting of protein or oil production, seed protein or oil production, insoluble sugar level, soluble sugar level, and starch composition.

6. The transgenic plant of claim 1, wherein the recombinant polynucleotide comprises a nucleotide sequence encoding a polypeptide of SEQ ID NO:860.

7. The transgenic plant of claim 1, wherein the recombinant polynucleotide comprises a nucleotide sequence encoding a polypeptide of SEQ ID NO:802.

8. The transgenic plant of claim 1, wherein the recombinant polynucleotide comprises a nucleotide sequence encoding a polypeptide of SEQ ID NO:240.

9. The transgenic plant of claim 1, wherein the recombinant polynucleotide comprises a nucleotide sequence encoding a polypeptide of SEQ ID NO:274.

10. The transgenic plant of claim 1, wherein the recombinant polynucleotide comprises a nucleotide sequence encoding a polypeptide of SEQ ID NO:558.

11. The transgenic plant of claim 1, wherein the recombinant polynucleotide comprises a nucleotide sequence encoding a polypeptide of SEQ ID NO:24.

12. The transgenic plant of claim 1, wherein the recombinant polynucleotide comprises a nucleotide sequence encoding a polypeptide of SEQ ID NO:1120.

13. The transgenic plant of claim 1, wherein the recombinant polynucleotide comprises a nucleotide sequence encoding a polypeptide of SEQ ID NO:44.

14. The transgenic plant of claim 1, wherein the recombinant polynucleotide comprises a nucleotide sequence encoding a polypeptide of SEQ ID NO:460.

15. The transgenic plant of claim 1, wherein the recombinant polynucleotide comprises a nucleotide sequence encoding a polypeptide of SEQ ID NO:286.

16. The transgenic plant of claim 1, wherein the recombinant polynucleotide comprises a nucleotide sequence encoding a polypeptide of SEQ ID NO:120.

17. The transgenic plant of claim 1, wherein the recombinant polynucleotide comprises a nucleotide sequence encoding a polypeptide of SEQ ID NO:130.

18. The transgenic plant of claim 1, wherein the recombinant polynucleotide comprises a nucleotide sequence encoding a polypeptide of SEQ ID NO:134.

19. The transgenic plant of claim 1, wherein the recombinant polynucleotide comprises a nucleotide sequence encoding a polypeptide of SEQ ID NO:698.

20. The transgenic plant of claim 1, wherein the recombinant polynucleotide comprises a nucleotide sequence encoding a polypeptide of SEQ ID NO:832.

21. The transgenic plant of claim 1, wherein the recombinant polynucleotide comprises a nucleotide sequence encoding a polypeptide of SEQ ID NO:580.

22. The transgenic plant of claim 1, wherein the recombinant polynucleotide comprises a nucleotide sequence encoding a polypeptide of SEQ ID NO:612.

23. The transgenic plant of claim 1, wherein the recombinant polynucleotide comprises a nucleotide sequence encoding a polypeptide of SEQ ID NO:48.

24. The transgenic plant of claim 1, wherein the recombinant polynucleotide comprises a nucleotide sequence of SEQ ID NO:859.

25. The transgenic plant of claim 1, wherein the recombinant polynucleotide comprises a nucleotide sequence of SEQ ID NO:801.

26. The transgenic plant of claim 1, wherein the recombinant polynucleotide comprises a nucleotide sequence of SEQ ID NO:239.

27. The transgenic plant of claim 1, wherein the recombinant polynucleotide comprises a nucleotide sequence of SEQ ID NO:273.

28. The transgenic plant of claim 1, wherein the recombinant polynucleotide comprises a nucleotide sequence of SEQ ID NO:557.

29. The transgenic plant of claim 1, wherein the recombinant polynucleotide comprises a nucleotide sequence of SEQ ID NO:23.

30. The transgenic plant of claim 1, wherein the recombinant polynucleotide comprises a nucleotide sequence of SEQ ID NO:1119.

31. The transgenic plant of claim 1, wherein the recombinant polynucleotide comprises a nucleotide sequence of SEQ ID NO:43.

32. The transgenic plant of claim 1, wherein the recombinant polynucleotide comprises a nucleotide sequence of SEQ ID NO:459.

33. The transgenic plant of claim 1, wherein the recombinant polynucleotide comprises a nucleotide sequence of SEQ ID NO:285.

34. The transgenic plant of claim 1, wherein the recombinant polynucleotide comprises a nucleotide sequence of SEQ ID NO:119.

35. The transgenic plant of claim 1, wherein the recombinant polynucleotide comprises a nucleotide sequence of SEQ ID NO:129.

36. The transgenic plant of claim 1, wherein the recombinant polynucleotide comprises a nucleotide sequence of SEQ ID NO:133.

37. The transgenic plant of claim 1, wherein the recombinant polynucleotide comprises a nucleotide sequence of SEQ ID NO:697.

38. The transgenic plant of claim 1, wherein the recombinant polynucleotide comprises a nucleotide sequence of SEQ ID NO:831.

39. The transgenic plant of claim 1, wherein the recombinant polynucleotide comprises a nucleotide sequence of SEQ ID NO:579.

40. The transgenic plant of claim 1, wherein the recombinant polynucleotide comprises a nucleotide sequence of SEQ ID NO:611.

41. The transgenic plant of claim 1, wherein the recombinant polynucleotide comprises a nucleotide sequence of SEQ ID NO:47.

42. The transgenic plant of claim 1, further comprising a constitutive, inducible, or tissue-specific promoter operably linked to said nucleotide sequence.

44. The transgenic plant of claim 1, wherein the plant is selected from the group consisting of: soybean, wheat, corn, potato, cotton, rice, oilseed rape, sunflower, alfalfa, sugarcane, turf, banana, blackberry, blueberry, strawberry, raspberry, cantaloupe, carrot, cauliflower, coffee, cucumber, eggplant, grapes, honeydew, lettuce, mango, melon, onion, papaya, peas, peppers, pineapple, pumpkin, spinach, squash, sweet corn, tobacco, tomato, watermelon, mint and other labiates, rosaceous fruits, and vegetable brassicas.

44. The transgenic plant of claim 1 wherein the encoded polypeptide is expressed and regulates transcription of a gene.

45. A method of using the transgenic plant of claim 1 to grow a progeny plant from a parent plant, the method comprising crossing the transgenic plant with another plant, selecting seed, and growing the progeny plant from the seed.

46. An isolated or recombinant polynucleotide comprising a nucleotide sequence selected from the group consisting of:
(a) a nucleotide sequence encoding a polypeptide comprising a sequence selected from SEQ ID NOs: 240, 274, 558, 286, 698, and 832, or a complementary nucleotide sequence thereof;
(b) a nucleotide sequence of SEQ ID NOs:239, 273, 557, 285, 697, 831, or a complementary nucleotide sequence thereof; and
(c) a nucleotide sequence that hybridizes under stringent conditions to a nucleotide sequence of one or more of: (a) or (b).

47. The isolated or recombinant polynucleotide of claim 46, wherein the recombinant polynucleotide comprises a nucleotide sequence encoding a polypeptide of SEQ ID NO:240.

48. The isolated or recombinant polynucleotide of claim 46, wherein the recombinant polynucleotide comprises a nucleotide sequence encoding a polypeptide of SEQ ID NO:274.

49. The isolated or recombinant polynucleotide of claim 46, wherein the recombinant polynucleotide comprises a nucleotide sequence encoding a polypeptide of SEQ ID NO:558.

50. The isolated or recombinant polynucleotide of claim 46, wherein the recombinant polynucleotide comprises a nucleotide sequence encoding a polypeptide of SEQ ID NO:286.

51. The isolated or recombinant polynucleotide of claim 46, wherein the recombinant polynucleotide comprises a nucleotide sequence encoding a polypeptide of SEQ ID NO:698.

52. The isolated or recombinant polynucleotide of claim 46, wherein the recombinant polynucleotide comprises a nucleotide sequence encoding a polypeptide of SEQ ID NO:832.

53. The isolated or recombinant polynucleotide of claim 46, wherein the recombinant polynucleotide comprises a nucleotide sequence of SEQ ID NO:239.

54. The isolated or recombinant polynucleotide of claim 46, wherein the recombinant polynucleotide comprises a nucleotide sequence of SEQ ID NO:273.

55. The isolated or recombinant polynucleotide of claim 46, wherein the recombinant polynucleotide comprises a nucleotide sequence of SEQ ID NO:557.

56. The isolated or recombinant polynucleotide of claim 46, wherein the recombinant polynucleotide comprises a nucleotide sequence of SEQ ID NO:285.

57. The isolated or recombinant polynucleotide of claim 46, wherein the recombinant polynucleotide comprises a nucleotide sequence of SEQ ID NO:697.

58. The isolated or recombinant polynucleotide of claim 46, wherein the recombinant polynucleotide comprises a nucleotide sequence of SEQ ID NO:831.

59. The isolated or recombinant polynucleotide of claim 46, further comprising a constitutive, inducible, or tissue-specific promoter operably linked to the nucleotide sequence.

60. The isolated or recombinant polynucleotide of claim 46 wherein the encoded polypeptide is expressed and regulates transcription of a gene.

61. A vector comprising the isolated or recombinant polynucleotide of claim 46.

62. A host cell comprising the vector of claim 61.

63. A method of using the isolated or recombinant polynucleotide of claim 46 for producing a plant having a modified trait, the method comprising selecting a polynucleotide that encodes a polypeptide, inserting the polynucleotide into an expression vector, introducing the vector into a plant or a cell of a plant to overexpress the polypeptide, thereby producing a modified plant, and selecting a modified plant for a modified trait.

64. The method of claim 63 wherein the plant possesses a modified trait as compared to another plant wherein the trait is an alteration in one or more physical characteristics selected from the group consisting of: the number of trichomes, fruit and seed size and number, yield of stems, leaves, inflorescences, or roots, stability of seeds during storage, susceptibility of the seed to shattering, root hair length and quantity, internode distances, or the quality of seed coat.

65. The method of claim 63 wherein the plant possesses a modified as compared to another plant wherein the trait is an alteration in a plant growth characteristic selected from the group consisting of: growth rate, germination rate of seeds, vigor of plants and seedlings, leaf and flower senescence, male sterility, apomixis, flowering time, flower abscission, rate of nitrogen uptake, osmotic sensitivity to soluble sugar concentrations, biomass or transpiration characteristics, apical dominance, branching patterns, number of organs, organ identity, and organ shape or size.

66. The method of claim 63 wherein the plant possesses a modified trait as compared to another plant wherein the trait is an alteration in one or more characteristics selected from the group consisting of protein or oil production, seed protein or oil production, insoluble sugar level, soluble sugar level, and starch composition.

67. A modified plant produced by the method of claim 63.

68. A method of using the plant of claim 67 to grow a progeny plant from a parent plant, the method comprising crossing the transgenic plant with another plant, selecting seed, and growing the progeny plant from the seed.

69. The plant produced by the method of claim 68.

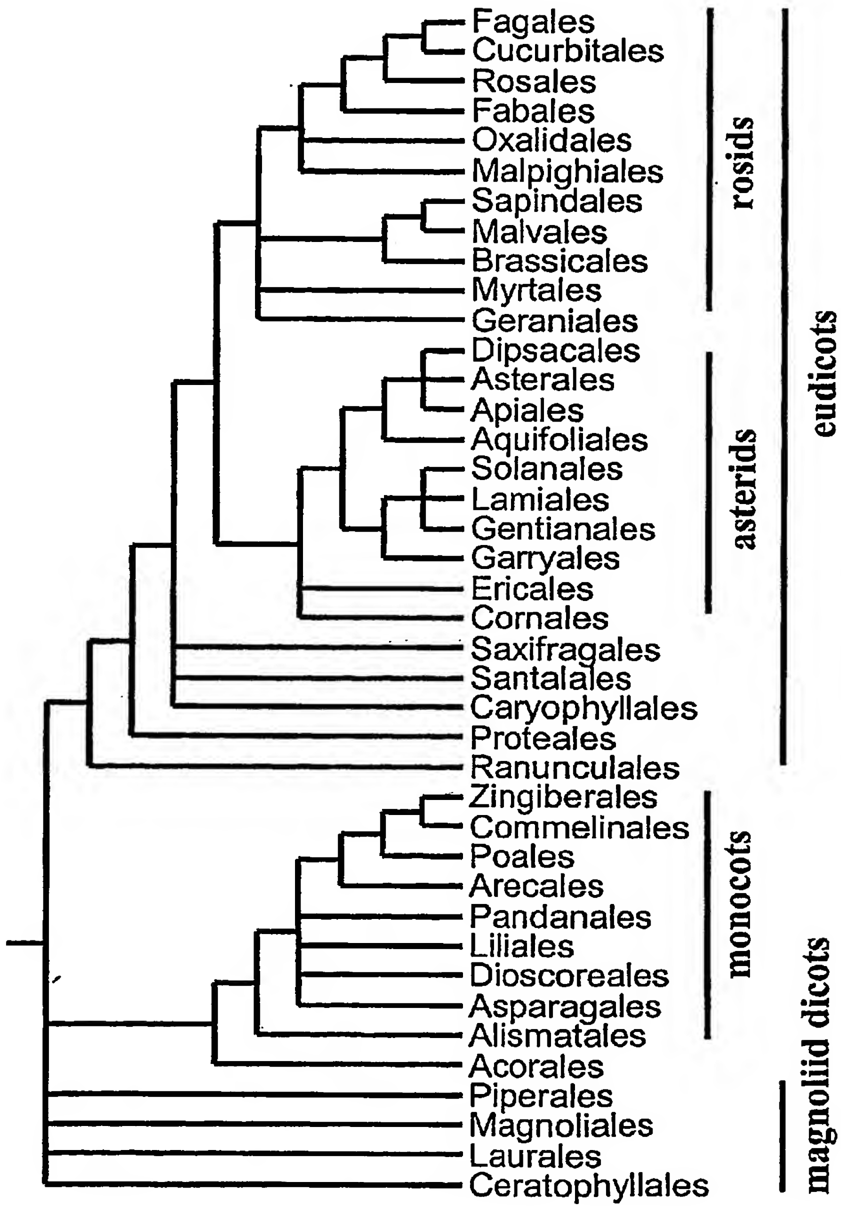
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Figure 1

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Ratcliffe, Oliver
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Adam, Luc J.
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Heard, Jacqueline E.
Pilgrim, Marsha L.
Jiang, Cai-Zhong
Reuber, T. Lynne
Creelman, Robert A.
Pineda, Omaira
Yu, Guo-Liang
Broun, Pierre E.

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>G2291 (27..797)
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>G2291 Amino Acid Sequence (domain in AA coordinates: TBD)
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KMGLELDLSLGLLSRK*
>G2452 (1..804)
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>G2452 Amino Acid Sequence (conserved domain in AA coordinates:27-213)

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>G2509 (143..934)

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>G2509 Amino Acid Sequence (domain in aa coordinates: 89-156)

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>G390 (1..2526)

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>G390 Amino Acid Sequence (domain in AA coordinates: 18-81)
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>G391 (1..2559)
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>G391 Amino Acid Sequence (domain in AA coordinates: 25-85)
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>G438 (188..2716)
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>G438 Amino Acid Sequence (domain in AA coordinates: 22-85)
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>G47 (38..472)
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>G47 Amino Acid Sequence (domain in AA coordinates: 11-80)
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>G559 (89..1285)
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>G559 Amino Acid Sequence (domain in AA coordinates: 203-264)
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>G568 (141..995)
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>G568 Amino Acid Sequence (domain in AA coordinates: 215-265)
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>G580 (43..747)
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>G580 Amino Acid Sequence (domain in AA coordinates:162-218)
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>G615 (197..1252)
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>G615 Amino Acid Sequence (domain in AA coordinates:88-147)
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>G732 (73..588)
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>G732 Amino Acid Sequence (domain in AA coordinates: 31-91)
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>G988 (1..1338)
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>G988 Amino Acid Sequence (domain in AA coordinates:178-195)
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>G1519 (1..1146)

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>G1519 Amino Acid Sequence (domain in AA coordinates: 327-364)

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>G374 (1..1359)

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>G374 Amino Acid Sequence (domain in aa coordinates: 35-67, 245-277)
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>G877 (397..2460)
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>G877 Amino Acid Sequence (domain in AA coordinates: 272-328, 487-603)

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GMEPKVEPVSDSGQSVYNQIMSRLPQI*

>G1000 (1..954)

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>G1000 Amino Acid Sequence (domain in AA coordinates: 14-117)

MGRPPCCDKSNVKKGLWTEEEDAKILAYVAIHGVGNWSLIPKKAGLNRCGKSCRLRWTNY
LRPDLKHDSFSTQEEELIIECHRAIGSRWSSIARKLPGRTDNDVKNHWNTKLKKKLMKMG
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SPMMFTNSSEYQTTPFHFYSHPNHLLNGTTSSCSSSSSSTSITQPNQVPQTPVTNFYWSD
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DQEMLSQFPQLLNDFDY*

>G1067 (436..1371)

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>G1067 Amino Acid Sequence (domain in AA coordinates: 86-93)
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SPGADIVESVSTYARRRGRGVSVLGGNGTVSNVTLRQPVTPGNGGGVSGGGGVVTLHGRF
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WGAGTPSRPPF*
>G1075 (19..876)
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AAAT
>G1075 Amino Acid Sequence (domain in AA coordinates: 78-85)
MAGLDLGTTSRYVHNVDGGGGGQFTTDNHHEDDGGAGGNHHHHHHNHNHHQGLDLIASND
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>G1266 (62..718)
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>G1266 Amino Acid Sequence (domain in AA coordinates: 79-147)
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>G1311 (41..757)
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TTTAAAAAAAAAAAAAAAAA
>G1311 Amino Acid Sequence (domain in AA coordinates: 11-112)
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PYENRISDWISEISTDQSEANLSEDHSSNSCSENNINIGTWWFQETRDFEEFSCSLWS*
>G1321 (72..803)
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>G1321 Amino Acid Sequence (domain in AA coordinates: 4-106)
MIMCSRGHWRPAEDEKLKDLVEQYGPHNWNAIALKLPGRSGKSCRLRWFNQLDPRINRNP
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SAS*
>G1326 (32..784)
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>G1326 Amino Acid Sequence (domain in AA coordinates: 18-121)
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IDFLGVGLAS*
>G1367 (128..1567)
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>G1367 Amino Acid Sequence (domain in AA coordinates: 179-201, 262-285, 298-319, 335-357)
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TPQTIKRGRGRPPKAKPDVVQPQPLTNGKLTWEQSELPVSRPEEIQIQPPQLPLQPQQPV
KRPPGRPRKDGTSPTVKPAASVSGGVETVKRRGRPPSGRAAGRERKPIVVSAPASVFPYV
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>G1386 (89..673)

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>G1386 Amino Acid Sequence (domain in AA coordinates: TBD)
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DSFPYEEPFLSQSY*
>G1421 (292..1155)
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>G1421 Amino Acid Sequence (domain in AA coordinates: 74-151)
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>G1453 (39..917)
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TGAGTGGAGAAGACTAAAAAAGGCTTTCCTATGCATGCATGCACTAGAAACGTCGTCGCA
TTTTGGATTTACATGCGGCCGCT

>G1453 Amino Acid Sequence (conserved domain in AA coordinates:13-160)
MMKVDQDYSCSIPPGFRFHPTDEELVGYYLKKKIASQRIDLDVIREIDLYKIEPWDLQER
CRIGYEEQTEWYFFSHRDKKYPTGTRTNRATVAGFWKATGRDKAVYLNSKLIGMRKTLVF
YRGRAPNGQKSDWIIHEYYSLESHQNSPPQEEGWVVCRAFKKRTTIPTKRRQLWDPNCLF
YDDATLLEPLDKRARHNPDFTATPFKQELLSEASHVQDGDFGSMYLQCIDDDQFSQLPQL
ESPSLPSEITPHSTTFSENSSRKDDMSSEKRITDWRYLDKFVASQFLMSGED*

>G1560 (120..1340)
ATCCTTTCAATTTCCACTCCTCTCTAATATAATTCACATTTTCCCACTATTGCTGATTCA
TTTTTTTTTGTGAATTATTTCAAACCCACATAAAAAAATCTTTGTTTAAATTTAAAACCA
TGGATCCTTCATTTAGGTTCATTAAAGAGGAGTTTCCTGCTGGATTCAGTGATTCTCCAT
CACCACCATCTTCTTCTTCATACCTTTATTCATCTTCCATGGCTGAAGCAGCCATAAATG
ATCCAACAACATTGAGCTATCCACAACCATTAGAAGGTCTCCATGAATCAGGGCCACCTC
CATTTTTGACAAAGACATATGACTTGGTGGAAGATTCAAGAACCAATCATGTCGTGTCTT
GGAGCAAATCCAATAACAGCTTCATTGTCTGGGATCCACAGGCCTTTTCTGTAACTCTCC
TTCCCAGATTCTTCAAGCACAATAACTTCTCCAGTTTTGTCCGCCAGCTCAACACATATG
GTTTCAGAAAGGTGAATCCGGATCGGTGGGAGTTTGCAAACGAAGGGTTTCTTAGAGGGC
AAAAGCATCTCCTCAAGAACATAAGGAGAAGAAAAACAAGTAATAATAGTAATCAAATGC
AACAACCTCAAAGTTCTGAACAACAATCTCTAGACAATTTTTGCATAGAAGTGGGTAGGT
ACGGTCTAGATGGAGAGATGGACAGCCTAAGGCGAGACAAGCAAGTGTTGATGATGGAGC
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AGCTCAAGAAGACCGAGTCAAAACAAAAACAAATGATGAGCTTCCTTGCCCGCGCAATGC
AGAATCCAGATTTTATTCAGCAGCTAGTAGAGCAGAAGGAAAAGAGGAAAGAGATCGAAG
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ATGGTGATGAAAGTGGTTATGGGAATGATGTTGCAGCCTCATCCTCAGCATTGATTGGTA
TGAGTCAGGAATATACATATGGAAACATGTCTGAATTCGAGATGTCGGAGTTGGACAAAC
TTGCTATGCACATTCAAGGACTTGGAGATAATTCCAGTGCTAGGGAAGAAGTCTTGAATG
TGGAAAAAGGAAATGATGAGGAAGAAGTAGAAGATCAACAACAAGGGTACCATAAGGAGA
ACAATGAGATTTATGGTGAAGGTTTTTGGGAAGATTTGTTAAATGAAGGTCAAAATTTTG
ATTTTGAAGGAGATCAAGAAAATGTTGATGTGTTAATTCAGCAACTTGGTTATTTGGGTT
CTAGTTCACACACTAATTAAGAAGAAATTGAAATGATGACTACTTTAAGCATTTGAATCA
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>G1560 Amino Acid Sequence (domain in AA coordinates: 62-151)
MDPSFRFIKEEFPAGFSDSPSPPSSSSYLYSSSMAEAAINDPTTLSYPQPLEGLHESGPP
PFLTKTYDLVEDSRTNHVVSWSKSNNSFIVWDPQAFSVTLLPRFFKHNNFSSFVRQLNTY
GFRKVNPDRWEFANEGFLRGQKHLLKNIRRRKTSNNSNQMQQPQSSEQQSLDNFCIEVGR
YGLDGEMDSLRRDKQVLMMELVRLRQQQQSTKMYLTLIEEKLKKTESKQKQMMSFLARAM
QNPDFIQQLVEQKEKRKEIEEAISKKRQRPIDQGKRNVEDYGDESGYGNDVAASSSALIG
MSQEYTYGNMSEFEMSELDKLAMHIQGLGDNSSAREEVLNVEKGNDEEEVEDQQQGYHKE
NNEIYGEGFWEDLLNEGQNFDFEGDQENVDVLIQQLGYLGSSSHTN*

>G1594 (1..984)
ATGGATGGAATGTACAATTTCCATTCGGCCGGTGATTATTCAGATAAGTCGGTTCTGATG
ATGTCACCGGAGAGTCTCATGTTTCCTTCCGATTACCAAGCTTTGCTATGTTCCTCCGCC
GGTGAAAATCGTGTCTCTGATGTTTTCGGATCCGACGAGCTACTCTCAGTAGCCGTCTCC
GCTTTGTCGTCGGAGGCGGCTTCGATCGCTCCGGAGATCCGAAGAAATGATGATAACGTT
TCTCTAACTGTCATCAAAGCTAAAATCGCTTGTCATCCTTCGTATCCTCGCTTACTTCAA
GCTTACATCGATTGCCAAAAAGGTCGGAGCACCACCGGAGATAGCGTGTTTACTAGAGGAG
ATTCAACGGGAGAGTGATGTTTATAAGCAAGAGGTTGTTCCTTCTTCTTGCTTTGGAGCT
GATCCTGAGCTTGATGAATTTATGGAAACGTACTGCGATATATTAGTGAAATACAAATCG

GATCTAGCAAGACCGTTTGACGAGGCAACGTGTTTCTTGAACAAGATTGAGATGCAGCTA
CGGAACCTATGTACTGGTGTCGAGTCTGCCAGGGGAGTTTCTGAGGATGGTGTAATATCA
TCTGACGAGGAACTGAGTGGAGGTGATCATGAGGTAGCAGAGGATGGGAGACAAAGATGT
GAAGACCGGGACCTCAAAGATAGGTTGCTACGCAAATTTGGAAGCCGTATTAGTACTTTA
AAGCTTGAGTTCTCAAAGAAGAAGAAGAAAGGAAAGTTACCAAGAGAAGCAAGACAAGCT
CTTCTTGATTGGTGGAATCTCCATTATAAGTGGCCTTACCCTACTGAAGGAGATAAGATA
GCATTAGCTGATGCAACGGGGTTAGACCAAAAACAAATCAACAATTGGTTTATAAACCAA
AGGAAACGTCATTGGAAGCCATCAGAGAATATGCCTTTCGCTATGATGGATGATTCTAGT
GGATCATTCTTTACCGAGGAATGA
>G1594 Amino Acid Sequence (conserved domain in AA coordinates:343-308)
MDGMYNFHSAGDYSDKSVLMMSPESLMFPSDYQALLCSSAGENRVSDVFGSDELLSVAVS
ALSSEAASIAPEIRRNDDNVSLTVIKAKIACHPSYPRLLQAYIDCQKVGAPPEIACLLEE
IQRESDVYKQEVVPSSCFGADPELDEFMETYCDILVKYKSDLARPFDEATCFLNKIEMQL
RNLCTGVESARGVSEDGVISSDEELSGGDHEVAEDGRQRCEDRDLKDRLLRKFGSRISTL
KLEFSKKKKKGKLPREARQALLDWWNLHYKWPYPTEGDKIALADATGLDQKQINNWFINQ
RKRHWKPSENMPFAMMDDSSGSFFTEE*
>G1750 (94..1101)
CCCTTTTCCTCTCTTTCTCCAAATCTCTGAAAATTTTCACCAGAATCTCTGTTCTTTTTT
TCACCAGAATCTCTCTGTTTAAAATAATAGGTGATGATGATGGATGAGTTTATGGATCTT
AGACCAGTGAAGTACACAGAGCACAAGACTGTTATCAGAAAGTACACTAAAAAGTCGTCT
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CGTGACGCCACTGATTCATCAAGCGACGAGGAAGAGTTTCTGTTCCCTCGAAGACGTGTC
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GCTTCTCCGACGAAGGACCGGAAAAGAATCAACGTTGATTCTACGGTTCAAAAGCCCTCT
GTTTCCGGCCAAAACCAGAAGAAGTACCGCGGCGTGAGACAGCGACCATGGGGAAAATGG
GCGGCGGAGATTCGTGATCCTGAGCAACGCCGGAGAATCTGGCTCGGTACTTTTGCAACG
GCGGAGGAAGCTGCCATCGTCTACGACAACGCAGCAATCAAACTTCGTGGCCCTGATGCT
CTTACCAACTTCACCGTACAACCAGAACCAGAACCGGTACAAGAACAAGAACAAGAACCG
GAGAGCAACATGTCGGTTTCGATATCAGAATCAATGGACGATTCTCAACATCTATCATCT
CCGACATCGGTTCTCAACTACCAAACATATGTCTCGGAGGAACCAATCGATAGTCTTATC
AAACCGGTTAAACAAGAGTTTCTTGAACCAGAACAAGAGCCAATAAGCTGGCATCTTGGA
GAAGGTAATACTAATACTAATGATGATTCATTTCCATTGGACATTACATTTCTCGACAAC
TATTTCAATGAATCATTACCAGACATCTCCATCTTCGATCAACCTATGTCTCCTATTCAA
CCAACAGAGAATGATTTCTTCAACGACCTTATGTTATTCGATAGCAACGCAGAAGAATAC
TACTCCTCCGAGATCAAAGAGATTGGTTCATCGTTCAACGATCTTGATGATTCTTTGATA
TCCGATCTCTTACTTGTGTGATATTTTTGCCATTAACCAAACACCGGTTTGGTTGC
>G1750 Amino Acid Sequence (domain in AA coordinates: 107-173)
MMMDEFMDLRPVKYTEHKTVIRKYTKKSSMERKTSVRDSARLVRVSMTDRDATDSSSDEE
EFLFPRRRVKRLINEIRVEPSSSSTGDVSASPTKDRKRINVDSTVQKPSVSGQNQKKYRG
VRQRPWGKWAAEIRDPEQRRRIWLGTFATAEEAAIVYDNAAIKLRGPDALTNFTVQPEPE
PVQEQEQEPESNMSVSISESMDDSQHLSSPTSVLNYQTYVSEEPIDSLIKPVKQEFLEPE
QEPISWHLGEGNTNTNDDSFPLDITFLDNYFNESLPDISIFDQPMSPIQPTENDFFNDLM
LFDSNAEEYYSSEIKEIGSSFNDLDDSLISDLLLV*
>G1947 (70..918)
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GTTCACAAAATGGATTATAACCTTCCAATTCCATTAGAGGGTCTCAAAGAAACGCCACCA
ACGGCTTTCTTGACGAAAACATACAACATAGTGGAGGATTCAAGCACAAACAACATAGTT
TCATGGAGCAGAGACAACAACAGCTTCATTGTTTGGGAACCAGAGACTTTTGCCCTAATT
TGCCTCCCTAGATGCTTTAAGCACAATAATTTCTCCAGCTTTGTTAGACAGCTCAATACT
TATGGGTTTAAGAAGATTGATACAGAGAGATGGGAATTTGCAAATGAGCATTTTCTGAAG
GGAGAGAGGCATCTTCTTAAGAACATCAAGAGAAGAAAGACATCATCTCAAACGCAAACG
CAGTCGCTAGAAGGAGAGATCCATGAGCTGCGAAGAGACAGAATGGCTTTAGAAGTAGAA
CTGGTTAGACTGCGACGAAAACAAGAAAGCGTGAAGACATATCTGCATTTGATGGAAGAG
AAACTGAAAGTCACAGAAGTAAAGCAAGAAATGATGATGAATTTCTTGCTAAAGAAGATT
AAGAAACCGAGTTTTTTACAGAGCTTAAGGAAACGTAATCTGCAAGGAATCAAGAATCGA
GAGCAAAAGCAAGAGGTGATCTCAAGCCATGGTGTTGAGGATAATGGAAAGTTTGTTAAA
GCTGAGCCAGAAGAGTATGGTGATGACATCGATGATCAATGTGGAGGTGTGTTTGATTAT

GGTGATGAGCTTCACATAGCTTCAATGGAGCATCAAGGACAAGGGGAGGATGAAATTGAA
ATGGATAGTGAAGGAATTTGGAAGGGTTTCGTGTTGAGTGAGGAGGAGATGTGTGATTTA
GTGGAACATTTTATATAATAAACTAATGTATTATGAGAGGTTTTTTTTGTTTTTTTGCT
TTTTTTTTCCGAGTTTGTCATCAAGCATTGTATACAATTTGGGCCAAACTAAAAGCCCAA
CAAAATATTTGGCCTTGGCATTTGTTAACAAATTGACTAATTCGGCCACACCTTCC
>G1947 Amino Acid Sequence (domain in AA coordinates: 37-120)
MDYNLPIPLEGLKETPPTAFLTKTYNIVEDSSTNNIVSWSRDNNSFIVWEPETFALICLP
RCFKHNNFSSFVRQLNTYGFKKIDTERWEFANEHFLKGERHLLKNIKRRKTSSQTQTQSL
EGEIHELRRDRMALEVELVRLRRKQESVKTYLHLMEEKLKVTEVKQEMMMNFLLKKIKKP
SFLQSLRKRNLQGIKNREQKQEVISSHGVEDNGKFVKAEPEEYGDDIDDQCGGVFDYGDE
LHIASMEHQGQGEDEIEMDSEGIWKGFVLSEEEMCDLVEHFI*
>G2011 (309..1547)
AATGTCGGTTGTACAATTATTTGTCACTAAAGTTTCCAAATTTCTTCTAAACTGATGAAT
CAATGGAACATGATGACGAAAAAGATAAATCCACGGTGGCGGGAACTGACCCACCCATTT
CCACCGCCTCTCTATTCCCCAGATTTTTTTCAATTATCTGACTACAGTTTGTCGGTTACT
TCCTTCCCTAAACCTTTATAAACCATTAAACCTCTCATCCTTCTTCTCTTAAACCCCCTA
ATTATCACACACACCCCAATTTCTCACTCTCTCTCTCACTAAAACCCGTAAATTTTCTAC
TATATCAAATGAGCCCAAAAAAAGATGCTGTTTCTAAACCAACTCCAATTTCAGTACCCG
TTTCGAGACGATCCGATATACCCGGGTCTCTCTACGTCGACACTGACATGGGTTTCTCTG
GGTCACCACTTCCCATGCCACTAGACATCTTACAAGGGAATCCAATTCCACCTTTTTTAT
CCAAGACTTTTGATTTGGTTGATGACCCGACTCTTGACCCGGTCATCTCTTGGGGACTGA
CCGGAGCTAGCTTCGTAGTTTGGGATCCTCTAGAGTTTGCCAGAATCATACTTCCAAGGA
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TTCTGAAGAACATTCATCGTCGTCGATCACCACAATCCAACCAAACTTGCTGCAGTAGCA
CTAGCCAAAGCCAAGGGTCACCTACTGAGGTTGGAGGAGAGATTGAGAAGCTGAGGAAAG
AGCGGCGTGCATTGATGGAGGAAATGGTTGAGCTTCAGCAGCAAAGCAGAGGCACAGCTC
GACATGTGGACACTGTAAACCAGAGGCTGAAAGCTGCAGAGCAACGTCAGAAGCAATTGC
TCTCTTTCTTGGCTAAGTTGTTTCAGAACCGGGGTTTCTTGGAACGCCTGAAGAACTTCA
AAGGAAAAGAAAAAGGAGGAGCTCTTGGATTGGAAAAGGCGAGAAAGAAGTTCATCAAGC
ACCACCAGCAGCCTCAAGATTCTCCAACAGGAGGGGAGGTGGTGAAGTATGAAGCTGATG
ATTGGGAGAGATTGCTAATGTATGACGAAGAGACTGAGAACACCAAGGGTTTAGGAGGGA
TGACTTCAAGCGATCCAAAAGGCAAGAACTTGATGTATCCATCAGAAGAAGAGATGAGCA
AACCAGATTACTTGATGTCCTTCCCATCTCCTGAAGGACTTATTAAACAAGAAGAGACGA
CATGGAGCATGGGTTTCGATACTACAATACCGAGTTTCAGCAACACCGATGCATGGGGAA
ACACAATGGACTATAATGATGTCTCAGAGTTTGGTTTTGCTGCAGAAACAACAAGTGATG
GTTTGCCTGATGTCTGCTGGGAACAATTTGCTGCAGGAATCACAGAGACTGGATTCAACT
GGCCAACTGGTGATGATGATGATAATACGCCAATGAATGATCCTTAGGATCTTTTCATAT
ATAGTTTAGACCAAAAACCCGTTTCTTATCGGGTGAACTATTAATTCATTATTCATTTTG
AATGCACTCTTTATACATATATATAATATTGATGAGTTTGATTGTTCCAAAAAAAAA
>G2011 Amino Acid Sequence (domain in AA coordinates: 56-147)
MSPKKDAVSKPTPISVPVSRRSDIPGSLYVDTDMGFSGSPLPMPLDILQGNPIPPFLSKT
FDLVDDPTLDPVISWGLTGASFVVWDPLEFARIILPRNFKHNNFSSFVRQLNTYGFRKID
TDKWEFANEAFLRGKKHLLKNIHRRRSPQSNQTCCSSTSQSQGSPTEVGGEIEKLRKERR
ALMEEMVELQQQSRGTARHVDTVNQRLKAAEQRQKQLLSFLAKLFQNRGFLERLKNFKGK
EKGGALGLEKARKKFIKHHQQPQDSPTGGEVVKYEADDWERLLMYDEETENTKGLGGMTS
SDPKGKNLMYPSEEEMSKPDYLMSFPSPEGLIKQEETTWSMGFDTTIPSFSNTDAWGNTM
DYNDVSEFGFAAETTSDGLPDVCWEQFAAGITETGFNWPTGDDDDNTPMNDP*
>G2094 (1..450)
ATGCTAGATCCCACCGAGAAAGTAATCGATTCAGAATCAATGGAAAGCAAACTCACATCA
GTAGATGCGATCGAAGAACACAGCAGCAGTAGCAGTAATGAAGCTATCAGCAACGAGAAG
AAGAGTTGTGCCATTTGTGGTACCAGCAAAACCCCTCTTTGGCGAGGCGGTCCTGCCGGT
CCCAAGTCGCTTTGTAACGCATGCGGGATCAGAAACAGAAAGAAAAGAAGAACACTGATC
TCAAATAGATCAGAAGATAAGAAGAAGAAGAGTCATAACAGAAACCCGAAGTTTGGTGAC
TCGTTGAAGCAGCGATTAATGGAATTGGGGAGAGAAGTGATGATGCAGCGATCAACGGCT
GAGAATCAACGGCGGAATAAGCTTGGCGAAGAAGAGCAAGCCGCCGTGTTACTCATGGCT
CTCTCTTATGCTTCTTCCGTTTATGCTTAA

>G2094 Amino Acid Sequence (domain in AA coordinates:43-68)
MLDPTEKVIDSESMESKLTSVDAIEEHSSSSNEAISNEKKSCAICGTSKTPLWRGGPAG
PKSLCNACGIRNRKKRRTLISNRSEDKKKKSHNRNPKFGDSLKQRLMELGREVMMQRSTA
ENQRRNKLGEEEQAAVLLMALSYASSVYA*
>G2113 (90..590)
ATAACAAACTCATCAAACTTCCTCAGCGTTTCTTTTTCTTACATAAACAATTTTTCTTAC
ATAAACAAATCTTGTTGTTTGTTGTTGTCATGGCACCGACAGTTAAAACGGCGGCCGTCA
AAACCAACGAAGGTAACGGAGTCCGTTACAGAGGAGTGAGGAAGAGACCATGGGGACGTT
ACGCAGCCGAGATCAGAGATCCTTTCAAGAAGTCACGTGTCTGGCTCGGTACTTTCGACA
CTCCTGAAGAAGCCGCTCGTGCCTACGACAAACGTGCTATTGAGTTTCGTGGAGCTAAAG
CCAAAACCAACTTCCCTTGTTACAACATCAACGCCCACTGCTTGAGTTTGACACAGAGCC
TGAGCCAGAGCAGCACCGTGGAATCATCGTTTCCTAATCTCAACCTCGGATCTGACTCTG
TTAGTTCGAGATTCCCTTTTCCTAAGATTCAGGTTAAGGCTGGGATGATGGTGTTCGATG
AAAGGAGTGAATCGGATTCTTCGTCGGTGGTGATGGATGTCGTTAGATATGAAGGACGAC
GTGTGGTTTTGGACTTGGATCTTAATTTCCCTCCTCCACCTGAGAACTGATTAAGATTTA
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>G2113 Amino Acid Sequence (domain in AA coordinates: TBD)
MAPTVKTAAVKTNEGNGVRYRGVRKRPWGRYAAEIRDPFKKSRVWLGTFDTPEEAARAYD
KRAIEFRGAKAKTNFPCYNINAHCLSLTQSLSQSSTVESSFPNLNLGSDSVSSRFPFPKI
QVKAGMMVFDERSESDSSSVVMDVVRYEGRRVVLDLDLNFPPPPEN*
>G2115 (41..733)
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GATCCAAACCAGCAGCACAAAAAAGGAAATGCCTTTGTCATCATCACCATCTTCTTCTTC
TTCTTCATCTTCTTCCTCGTCTTCGTCTTCGTGTAAGAACAAGAACAAGAAGAGTAAGAT
TAAGAAGTACAAAGGAGTGAGGATGAGAAGTTGGGGATCATGGGTCTCTGAGATTAGGGC
ACCAAATCAAAAGACAAGGATTTGGTTAGGTTCTTACTCAACAGCTGAAGCAGCTGCTAG
AGCTTACGATGTTGCACTCTTATGTCTCAAAGGCCCTCAAGCCAATCTCAACTTCCCTAC
TTCTTCTTCTTCTCATCATCTTCTTGATAATCTCTTAGATGAAAATACCCTTTTGTCCCC
CAAATCCATCCAAAGAGTAGCTGCTCAAGCTGCCAACTCATTTAACCATTTTGCCCCTAC
TTCATCAGCCGTCTCGTCACCGTCCGATCATGATCATCACCATGATGATGGGATGCAATC
TTTGATGGGATCTTTTGTGGACAATCATGTGTCTTTGATGGATTCAACATCTTCATGGTA
TGATGATCATAATGGGATGTTCTTGTTTGATAATGGAGCTCCATTCAATTACTCTCCTCA
ACTAAACTCGACGACGATGCTCGATGAATACTTCTACGAAGATGCTGACATTCCGCTTTG
GAGTTTCAATTAATCCGACGGTCCATAATACATACTTTAATTAGT
>G2115 Amino Acid Sequence (conserved domain in AA coordinates:46-115)
MVKQERKIQTSSTKKEMPLSSSPSSSSSSSSSSSSSCKNKNKKSKIKKYKGVRMRSWGS
WVSEIRAPNQKTRIWLGSYSTAEAAARAYDVALLCLKGPQANLNFPTSSSSHHLLDNLLD
ENTLLSPKSIQRVAAQAANSFNHFAPTSSAVSSPSDHDHHHDDGMQSLMGSFVDNHVSLM
DSTSSWYDDHNGMFLFDNGAPFNYSPQLNSTTMLDEYFYEDADIPLWSFN*
>G2130 (41..988)
CCTCTCTTCATTTTTTAACTCCCTCTCTCTCTCTCTCTCTATGGAGAGACGAACGAGACG
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TCCGAGACTGGTCCGTATCACTGTTACTGATCCTTTCGCTACTGACTCGTCTAGCGACGA
CGACGACAACAACAACGTCACGGTGGTTCCAAGAGTGAAACGATACGTGAAGGAGATTAG
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GGAAAGCGTAGTGGTTGAAGATGACGTGTCGACGTCGGTGAAGCCTAAAAAGTACAGAGG
CGTGAGACAGAGACCTTGGGGAAAATTCGCGGCGGAGATTAGAGATCCGTCGAGCCGTAC
TCGGATTTGGCTTGGGACTTTTGTCACGGCGGAGGAAGCTGCTATAGCGTACGATAGAGC
CGCGATTCATCTCAAAGGACCTAAAGCGCTCACGAATTTCCTAACTCCGCCGACGCCAAC
GCCGGTTATCGATCTCCAAACGGTTTCCGCCTGCGATTACGGTAGAGATTCTCGGCAGAG
CCTTCATTCACCGACCTCTGTTCTAAGATTCAACGTCAACGAGGAAACAGAGCATGAGAT
TGAAGCGATCGAGCTATCTCCGGAGAGAAAGTCGACGGTTATAAAAGAAGAAGAAGAATC
GTCGGCGGGTTTGGTGTTCCCGGATCCGTATCTGTTACCGGATTTATCTCTCGCCGGCGA
ATGTTTTTGGGATACCGAAATTGCCCCTGACCTTTTGTTTCTCGATGAAGAAACCAAAAT
CCAATCAACGTTGTTACCAAACACAGAGGTTTCGAAACAAGGAGAAAACGAAACTGAAGA
TTTCGAGTTTGGTTTGATTGATGATTTCGAGTCTTCTCCATGGGATGTGGATCATTTCTT
CGACCATCATCATCACTCTTTCGATTAAAAATCTCTTCTTTTTTGGGGAAATTTTTGTG

>G2130 Amino Acid Sequence (domain in AA coordinates 93-160)
MERRTRRVKFTENRTVTNVAATPSNGSPRLVRITVTDPFATDSSSDDDDNNNVTVVPRVK
RYVKEIRFCQGESSSSTAARKGKHKEEESVVVEDDVSTSVKPKKYRGVRQRPWGKFAAEI
RDPSSRTRIWLGTFVTAEEAAIAYDRAAIHLKGPKALTNFLTPPTPTPVIDLQTVSACDY
GRDSRQSLHSPTSVLRFNVNEETEHEIEAIELSPERKSTVIKEEEESSAGLVFPDPYLLP
DLSLAGECFWDTEIAPDLLFLDEETKIQSTLLPNTEVSKQGENETEDFEFGLIDDFESSP
WDVDHFFDHHHHSFD*

>G2147 (162..1262)
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TTGTCAGTTTATTCTCTGCAAACGTGCGGCCTAAGTAACACATGTCGAATTATGGAGTTA
AAGAGCTCACATGGGAAAATGGGCAACTAACCGTTCATGGTCTAGGCGACGAAGTAGAAC
CAACCACCTCGAATAACCCTATTTGGACTCAAAGTCTCAACGGTTGTGAGACTTTGGAGT
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AAGAAATGGACCGATGGTTCGCTGTTCAAGAGGAGAGCCATAGAGTTGGCCACAGCGTCA
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AGACAGCTAGAACCGGAGACAGAGACTATTTCCGCTCTGGATCGGAAACTCAAGATACTG
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CAGCAGCGATTCACAACGAGTCCGAAAGGAGACGGCGTGATAGGATAAACCAGAGGATGA
GAACACTTCAGAAGCTGCTTCCTACTGCAAGTAAGGCGGATAAAGTCTCAATCTTGGATG
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AACACCAACAACAACAACAACAACAGCAGCAGCAGCAGCAACAACAGCAGCAACAGTTTC
AGATGTCGTTGCTTGCAACAATGGCAAGAATGGGAATGGGAGGTGGTGGAAATGGTTATG
GAGGTTTAGTTCCTCCTCCTCCTCCTCCACCAATGATGGTCCCTCCTATGGGTAACAGAG
ACTGCACCAACGGTTCTTCAGCCACATTATCTGATCCATACAGCGCCTTTTTCGCACAGA
CAATGAATATGGATCTCTACAATAAAATGGCAGCAGCTATCTATAGACAACAGTCTGATC
AAACAACAAAGGTAAATATCGGCATGCCTTCAAGTTCTTCGAATCATGAGAAAAGAGATT
AGTCTAGCGACCTAGTATTATTGATCCATATATATAGTTCTTGAAAGATTGTTGTATCAT
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>G2147 Amino Acid Sequence (domain in AA coordinates:160-234)
MSNYGVKELTWENGQLTVHGLGDEVEPTTSNNPIWTQSLNGCETLESVVHQAALQQPSKF
QLQSPNGPNHNYESKDGSCSRKRGYPQEMDRWFAVQEESHRVGHSVTASASGTNMSWASF
ESGRSLKTARTGDRDYFRSGSETQDTEGDEQETRGEAGRSNGRRGRAAAIHNESERRRRD
RINQRMRTLQKLLPTASKADKVSILDDVIEHLKQLQAQVQFMSLRANLPQQMMIPQLPPP
QSVLSIQHQQQQQQQQQQQQQQQQQFQMSLLATMARMGMGGGGNGYGGLVPPPPPPPMMV
PPMGNRDCTNGSSATLSDPYSAFFAQTMNMDLYNKMAAAIYRQQSDQTTKVNIGMPSSSS
NHEKRD*

>G2156 (384..1292)
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CTCGGGTGAAGAATCTCTCCTCTCTTGCCCTAAAGCGAGTTAGGGTTTAACACACAAAGC
ATACCCTTTAGATTTGTGTCTCTTAGCTCTGTTTTTGTCGGCTTGTGTAACCGATCAACT
CAAGCTATTGGCTCCTCACCTCCTGAAATTTGACTTCTCCAATGGATCTCAAAGTTTCTC
TTATATGAATTCTATCTTCACCCTCACAATATCTTTATATATATGAGCCACAAGAACAAG
AAGAGTCAGTAGATGCGGCTGCCATGGACGGTGGTTACGATCAATCCGGAGGAGCTTCTA
GATACTTTCACAACCTCTTCAGGCCTGAGCTTCATCACCAGCTTCAACCTCAGCCTCAAC
TTCACCCTTTGCCTCAGCCTCAGCCTCAACCTCAGCCTCAGCAGCAGAATTCAGATGATG
AATCTGACTCCAACAAGGATCCGGGTTCCGACCCAGTTACCTCTGGTTCAACCGGGAAAC
GTCCACGTGGACGTCCTCCGGGATCCAAGAACAAGCCGAAGCCACCGGTGATAGTGACTA
GAGATAGCCCCAACGTGCTTAGATCTCATGTTCTTGAAGTCTCATCTGGAGCCGACATAG
TCGAGAGCGTTACCACTTACGCTCGCAGGAGAGGAAGAGGAGTCTCCATTCTCAGTGGTA
ACGGCACGGTGGCTAACGTCAGTCTCCGGCAGCCGGCAACGACAGCGGCTCATGGGGCAA
ATGGTGGAACCGGAGGTGTTGTGGCTCTACATGGAAGGTTTGAGATACTTTCCCTCACAG
GTACGGTGTTGCCGCCCCCTGCGCCGCCAGGATCCGGTGGTCTTTCTATCTTTCTTTCCG
GCGTTCAAGGTCAGGTGATTGGAGGAAACGTGGTGGCTCCGCTTGTGGCTTCGGGTCCAG

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>G2156 Amino Acid Sequence (domain in AA coordinates:66-86)
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>G2294 (24..659)
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>G2294 Amino Acid Sequence (conserved domain in AA coordinates:32-102)
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>G2510 (16..594)
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>G2510 Amino Acid Sequence (conserved domain in AA coordinates:41-108)
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>G2893 (130..981)
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>G2893 Amino Acid Sequence (conserved domain in AA coordinates:19-120)
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>G340 (97..834)
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>G340 Amino Acid Sequence (domain in AA coordinates: 37-154)
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SELVD*
>G39 (75..638)
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CTTGTCTTTGAACTTGTTTTATTTAGCATGCAAA
>G39 Amino Acid Sequence (domain in AA coordinates: 24-90)
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DWINNLI*
>G439 (128..967)
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>G439 Amino Acid Sequence (domain in AA coordinates: 110-177)
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>G470 (1..2580)
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>G470 Amino Acid Sequence (domain in AA coordinates: 61-393)
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>G652 (1..606)
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>G652 Amino Acid Sequence (domain in AA coordinates:28-49, 137-151, 182-196)
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>G671 (61..1119)
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>G671 Amino Acid Sequence (domain in AA coordinates: 15-115)
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>G779 (110..712)
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>G779 Amino Acid Sequence (domain in AA coordinates: 126-182)
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>G962 (148..1392)
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GAAACTGCCATTGTTGACGATCTTCAAAGACTAGTTAACTACCAAATATCAGATGGAGGT
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CCTTTTAAGTAATTTAATTAGATCATGATTATTATCCATGACAATAATTAATGCTGCTTT
GCGC
>G962 Amino Acid Sequence (domain in AA coordinates: 53-175)
MAIVSSTTSIIPMSNQVNNNEKGIEDNDHRGGQESHVQNEDEADDHDHDMVMPGFRFHPT
EEELIEFYLRRKVEGKRFNVELITFLDLYRYDPWELPAMAAIGEKEWYFYVPRDRKYRNG
DRPNRVTTSGYWKATGADRMIRSETSRPIGLKKTLVFYSGKAPKGTRTSWIMNEYRLPHH
ETEKYQKAEISLCRVYKRPGVEDHPSVPRSLSTRHHNHNSSTSSRLALRQQQHHSSSSNH
SDNNLNNNNNINNLEKLSTEYSGDGSTTTTTTNSNSDVTIALANQNIYRPMPYDTSNNTL
IVSTRNHQDDDETAIVDDLQRLVNYQISDGGNINHQYFQIAQQFHHTQQQNANANALQLV
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>G977 (46..591)
CACCAAACTCACCTGAAACCCTATTTCCATTTACCATTCACACTAATGGCACGACCACAA
CAACGCTTTCGAGGCGTTAGACAGAGGCATTGGGGCTCTTGGGTCTCCGAAATTCGTCAC
CCTCTCTTGAAAACAAGAATCTGGCTAGGGACGTTTGAGACAGCGGAGGATGCAGCAAGG
GCCTACGACGAGGCGGCTAGGCTAATGTGTGGCCCGAGAGCTCGTACTAATTTCCCATAC
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CTCCACAAATGCTACATGGCTTCTCTTCAAATGACCAAGCAAACGCAAACACAAACGCAA
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>G977 Amino Acid Sequence (domain in AA coordinates: 5-72)
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L*
>G1063 (241..966)
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GGTTTACTCACTAACCCTTCTTCTATCTCTCCCAACACAGCTTACTCTTCCGTTTTTCTT
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AGATGATGATGATTTTTAATTTTATTATTATTATATTAATGTTGGAGAAAAAGAGAAAAA
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CGAGTTTG
>G1063 Amino Acid Sequence (domain in aa coordinates: 131-182)
MDSDIMNMMMHQMEKLPEFCNPNSSFFSPDHNNTYPFLFNSTHYQSDHSMTNEPGFRYGS
GLLTNPSSISPNTAYSSVFLDKRNNSNNNNNGTNMAAMREMIFRIAVMQPIHIDPEAVKP
PKRRNVRISKDPQSVAARHRRERISERIRILQRLVPGGTKMDTASMLDEAIHYVKFLKKQ
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R*
>G1140 (67..729)
ATCCAAGATCCTCCAACTCACAGAAAGGCAGATTCAAGAACAGTAGTGAAGGAGAGATCT
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TGCGATGCTGATGTTGCTCTCATCATCTTCTCTGCCACCGGAAAGCTCTTCGAGTTCTCC
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TGGGAATGAATCTGAGAGAGAGAAAGATCCAGCAGAGTTGACTTCGATGGAAGCCCACAA
ATATTAAGTCTACCTTTTCCCTTTCTTTTCTTTGAATAAGTGTTGAAAAAGAATTGAGAT
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>G1140 Amino Acid Sequence (conserved domain in AA coordinates:2-57)
MAREKIRIKKIDNITARQVTFSKRRRGIFKKADELSVLCDADVALIIFSATGKLFEFSSS
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LEELQRLEKLLESGLSRVSEKKGECVMSQIFSLEKRGSELVDENKRLRDKLETLERAKLT
TLKEALETESVTTNVSSYDSGTPLEDDSDTSLKLGLPSWE*
>G1425 (43..1005)
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GCGATCATCGCCGACGTTGATCTTTACAAATTTGATCCATGGGAACTTCCCGCGAAAGCT
TCGTTTGGAGAACAAGAATGGTATTTTTTCAGTCCAAGAGATCGGAAATATCCCAACGGA
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GATGATCGATTCCGTCATGTTCCTCCTGGTCTTCACTTCCCGGCGATTTTTTCTGACAAT
AATGATCCGACGGCTATATATGATGGTGGCGGCGGCGGATACGGAGGTGGAAGTTACTCG
ATGAATCATTGTTTCGCATCTGGATCAAAGCAGGAGCAGTTGTTTCCACCGGTGATGATG
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CAAGGTGGGATTTACCAATTGCCTGGTTTGAATTGGTATTCTTGAAAACAATTTACGATG
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TTGGAGGAAAAAAAAAAAAAAAA
>G1425 Amino Acid Sequence (domain in AA coordinates: 20-173)
MESTDSSGGPPPPQPNLPPGFRFHPTDEELVIHYLKRKADSVPLPVAIIADVDLYKFDPW
ELPAKASFGEQEWYFFSPRDRKYPNGARPNRAATSGYWKATGTDKPVISTGGGGSKKVGV
KKALVFYSGKPPKGVKSDWIMHEYRLTDNKPTHICDFGNKKNSLRLDDWVLCRIYKKNNS
TASRHHHHLHHIHLDNDHHRHDMMIDDDRFRHVPPGLHFPAIFSDNNDPTAIYDGGGGGY
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TPLMQNQGGIYQLPGLNWYS*
>G1449 (105..581)
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>G1449 Amino Acid Sequence (domain in AA coordinates: 48-53,74-107,122-152)
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HVLTYEDKDGDWMMVGDIPWDMFLETVRRLKITRPERY*
>G1897 (1..678)
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AACACCAAGTTCTGTTACTACAACAACTACAACTTCTCACAACCTCGTCATTTCTGCAAG
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>G1897 Amino Acid Sequence (domain in AA coordinates:34-62)
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SCRRYWTHGGTLRDIPVGGVSRKSSKRSRTYSSAATTSVVGSRNFPLQATPVLFPQSSSN
GGITTAKGSASSFYGGFSSLINYNAAVSRNGPGGGFNGPDAFGLGLGHGSYYEDVRYGQG
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>G2143 (89..784)
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TGTTCCCGGTGGGACTAAGATGGATACGGCGTCGATGCTCGATGAGGCTATCCATTACGT

TAAGTTTCTCAAGAAGCAAGTGCAGTCGCTGGAGGAACATGCGGTGGTTAACGGCGGAGG
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>G2143 Amino Acid Sequence (domain in aa coordinates: 128-179)
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KNVRISKDPQSVAARHRRERISERIRILQRLVPGGTKMDTASMLDEAIHYVKFLKKQVQS
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>G2535 (1..1005)
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GACAAGACCATATATACCAATGGTGATAGAATCGGGATGCGAAAGACGCTTGTCTTCTAC
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TCAATACCAGCCGTTAATGAGACTTCACAATCACCGTATCATGGACTGAACCGGTCCGGT
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GATTTCGCGAGAACGACATGCCACTTGTTGAACGGTAGTGGATAA
>G2535 Amino Acid Sequence (conserved domain in AA coordinates:11-114)
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KGRAPHGQKSDWIMHEYRLDESVLISSCGDHDVNVETCDVIGSDEGWVVCRVFKKNNLCK
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LIDDQVNNCHVSKVMDPSFITSWAALDRLVASQLNGPNSYSIPAVNETSQSPYHGLNRSG
CNTGLTPDYYIPEIDLWNEADFARTTCHLLNGSG*
>G2557 (94..1215)
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GT
>G2557 Amino Acid Sequence (domain in aa coordinates: 278-328)
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PLQNPNQIHHPEC*
>G259 (52..786)
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CACCATGAGGATCAACAGTCTTCCGCCACTTCATCCTCTTTCGTATACACTGCATTACTC
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>G259 Amino Acid Sequence (domain in AA coordinates: 27-131)
MEDAGEHLRCNDNVNDEERLPLEFMIGNSTSTAELQPPPPFLVKTYKVVEDPTTDGVISW
NEYGTGFVVWQPAEFARDLLPTLFKHCNFSSFVRQLNTYGFRKVTTIRWEFSNEMFRKGQ
RELMSNIRRRKSQHWSHNKSNHQVVPTTTMVNQEGHQRIGIDHHHEDQQSSATSSSFVYT
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VKLE*
>G353 (82..570)
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>G353 Amino Acid Sequence (domain in aa coordinates: 41-61, 84-104)
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HKKPNNDALSSGLMKKVKTSSHPCPICGVEFPMGQALGGHMRRHRNESGAAGGALVTRAL
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>G354 (27..533)

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>G1792 Amino Acid Sequence (domain in aa coordinates: 17-85)
MESSNRSSNNQSQDDKQARFRGVRRRPWGKFAAEIRDPSRNGARLWLGTFETAEEAARAY
DRAAFNLRGHLAILNFPNEYYPRMDDYSLRPPYASSSSSSSSGSTSTNVSRQNQREVFEF
EYLDDKVLEELLDSEERKR*
>G1865 (48..899)
AAGAAGAGGACATGAAGCACAGAGATTCTGCAGACTGCAGGTGACCAATGGACACTTTAT
CAATAAAAACATACCTACTACTCTCTTACACTTTCAATTTTCCAATACAAATCCCAATCT
TTAATCTCTCTTTCTTCTTCATCTCTCTTTCTCTTTCTCTCTTCATGGCTACAAGGATTC
CATTCACAGAATCACAATGGGAAGAACTTGAAAACCAAGCTCTTGTGTTCAAGTACTTAG
CTGCAAATATGCCTGTTCCACCTCATCTTCTCTTCCTCATCAAAAGACCCTTTCTCTTCT
CTTCTTCTTCTTCTTCATCTTCTTCTTCAAGCTTCTTCTCTCCCACTCTTTCTCCACACT
TTGGGTGGAATGTGTATGAGATGGGAATGGGAAGAAAGATAGATGCAGAGCCAGGAAGAT
GTAGAAGAACTGATGGCAAGAAATGGAGATGCTCTAAAGAAGCTTACCCTGACTCTAAGT
ACTGTGAGAGACATATGCATAGAGGCAAGAACCGTTCTTCCTCAAGAAAGCCTCCTCCTA
CTCAATTCACTCCAAATCTCTTTCTCGACTCTTCTTCCAGAAGAAGAAGAAGTGGATACA
TGGATGATTTCTTCTCCATAGAACCTTCCGGGTCAATCAAAAGCTGCTCTGGCTCAGCAA

TGGAAGATAATGATGATGGCTCATGTAGAGGCATCAACAACGAGGAGAAGCAGCCGGATC
GACATTGCTTCATCCTTGGTACTGACTTGAGGACACGTGAGAGGCCATTGATGTTAGAGG
AGAAGCTGAAACAAAGAGATCATGATAATGAAGAAGAGCAAGGAAGCAAGAGGTTTTATA
GGTTTCTTGATGAATGGCCTTCTTCTAAATCTTCTGTTTCTACTTCACTCTTCATTTGAT
CATCTTTTGTTCTTATAACCTTGTATTTCTTGTTAAGATGGTAATGCAAATT
>G1865 Amino Acid Sequence (domain in AA coordinates: 124-149)
MDTLSIKTYLLLSYTFNFPIQIPIFNLSFFFISLSLSLFMATRIPFTESQWEELENQALV
FKYLAANMPVPPHLLFLIKRPFLFSSSSSSSSSSFFSPTLSPHFGWNVYEMGMGRKIDA
EPGRCRRTDGKKWRCSKEAYPDSKYCERHMHRGKNRSSSRKPPPTQFTPNLFLDSSSRRR
RSGYMDDFFSIEPSGSIKSCSGSAMEDNDDGSCRGINNEEKQPDRHCFILGTDLRTRERP
LMLEEKLKQRDHDNEEEQGSKRFYRFLDEWPSSKSSVSTSLFI*
>G1886 (43..909)
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ATCTCAAACGAGACTTTGGAAACTATATTGGTAAGTTCAACAAAAGGAAGCAATAATAAC
AATAAGAAAATGGAAGAAGAAATGAAGAAGAAAGTATCAAGAGGAGAATTAGGAGGTGAA
GCTCAAAATTGTCCAAGATGTGAATCTCCAAACACAAAGTTTTGTTACTACAACAACTAT
AGTCTCTCACAACCTCGTTACTTCTGCAAATCTTGTCGGAGATATTGGACTAAAGGCGGT
ACTCTTCGTAACGTTCCCGTCGGTGGTGGTTGCCGTCGAAACAAACGATCCTCTTCCTCA
GCTTTCTCCAAGAACAACAACAATAAGTCTATTAATTTCCATACTGATCCACTTCAGAAC
CCTTTAATTACGGGAATGCCACCATCATCTTTTGGTTATGATCACTCCATTGATCTCAAC
CTCGCTTTCGCTACTCTCCAAAAGCATCATTTATCCTCTCAAGCTACTACGCCTTCTTTT
GGGTTTGGAGGTGATCTTTCTATTTATGGAAACTCAACGAATGATGTAGGGATCTTCGGA
GGGCAAAACGGTACTTATAACAATAGTTTGTGTTATGGGTTTATGTCCGGAAATGGTAAT
AATAATCAAAATGAAATCAAGATGGCTTCTACATTGGGGATGTCTTTGGAAGGAAACGAG
AGAAAGCAAGAGAATGTGAACAATAACAATAATAACTCAGAGAATCCTAGCAAGGTGTTC
TGGGGGTTTCCATGGCAGATGACCGGAGATTCCGCCGGAGTTGTACCGGAGATTGATCCC
GGAAGGGAAAGCTGGAATGGGATGGTTTCATCTTGGAATAATGGTTTACTCAACACTCCT
TTGGTCTAGCAGATCATTAA
>G1886 Amino Acid Sequence (domain in aa coordinates: 17-59)
MDPEQEISNETLETILVSSTKGSNNNNKKMEEEMKKKVSRGELGGEAQNCPRCESPNTKF
CYYNNYSLSQPRYFCKSCRRYWTKGGTLRNVPVGGGCRRNKRSSSSAFSKNNNNKSINFH
TDPLQNPLITGMPPSSFGYDHSIDLNLAFATLQKHHLSSQATTPSFGFGGDLSIYGNSTN
DVGIFGGQNGTYNNSLCYGFMSGNGNNNQNEIKMASTLGMSLEGNERKQENVNNNNNNSE
NPSKVFWGFPWQMTGDSAGVVPEIDPGRESWNGMVSSWNNGLLNTPLV*
>G1933 (33..1418)
AATTGAGATTAAAGTAATTTATCTTTCAGAAAATGGCGGTTGAAGACGATGTATCTTTGA
TAAGAACGACGACGTTAGTGGCACCAACAAGACCCACGATTACAGTTCCTCATAGACCTC
CGGCGATCGAAACGGCGGCGTATTTCTTTGGCGGTGGAGATGGGCTTAGTCTAAGCCCAG
GGCCACTTTCTTTTGTCTCTTCTTTGTTTGTTGATAACTTCCCTGACGTCTTGACGCCGG
ATAACCAACGGACGACGTCGTTTACTCAGCTTCTTAACGGAACTATGTCGGTGTCTCCTG
GTGGCGGAGGACGTTCAACGGCGGGGATGTTCGCCGGAGGAGGTCCGATGTTTACAATCC
CTTCTGGTTTCAGCCCTTCTAGTCTTCTCACCTCGCCCATGTTCTTTCCCCCGCAGTCGT
CAGCTCATACCGGCTTTATTCAACCACGGCAGCAGTCACAACCGCAACCACAACGACCAG
ACACGTTTCCTCACCATATGCCACCATCGACATCCGTCGCCGTCCATGGTCGTCAATCTT
TAGACGTTTCACAAGTAGATCAAAGAGCTCGAAACCATTATAATAATCCGGGGAATAACA
ATAATAACCGGTCGTATAACGTTGTGAACGTTGATAAACCGGCGGATGACGGTTATAACT
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GTACACATGTTAACTGTCCGGTGAAGAAGAAAGTCGAACGGTCATCGGATGGACAGATCA
CTCAGATCATTTACAAAGGTCAACATGATCACGAGAGGCCTCAGAATCGCCGTGGCGGTG
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CGGCTTCAAAGATAAGAAGAATAGACGGTGTGTCGACGACTCACCGGACGGTGACCGAGC
CTAAGATTATCGTTCAGACAAAAAGTGAAGTCGATCTTCTCGACGATGGCTATAGGTGGC
GTAAGTACGGACAAAAAGTTGTCAAAGGAAATCCCCATCCAAGGAGCTATTATAAATGTA
CAACGCCAAATTGTACGGTCCGTAAACATGTAGAGAGAGCTTCCACGGATGCTAAGGCTG
TGATTACAACTTACGAAGGTAAACACAATCACGATGTCCCTGCCGCTAGAAACGGTACCG
CGGCAGCAACCGCAGCTGCGGTGGGGCCGTCTGACCACCATCGTATGAGATCAATGTCGG

GGAACAATATGCAACAACATATGAGTTTCGGTAACAATAATAACACAGGCCAATCTCCGG
TTCTTTTGAGGTTGAAAGAAGAGAAAATCACAATTTGACTTTTAAGAACCAAAGATTTCG
AGATTGATATT
>G1933 Amino Acid Sequence (conserved domain in AA coordinates:205-263, 344-404)
MAVEDDVSLIRTTTLVAPTRPTITVPHRPPAIETAAYFFGGGDGLSLSPGPLSFVSSLFV
DNFPDVLTPDNQRTTSFTQLLNGTMSVSPGGGGRSTAGMFAGGGPMFTIPSGFSPSSLLT
SPMFFPPQSSAHTGFIQPRQQSQPQPQRPDTFPHHMPPSTSVAVHGRQSLDVSQVDQRAR
NHYNNPGNNNNNRSYNVVNVDKPADDGYNWRKYGQKPIKGCEYPRSYYKCTHVNCPVKKK
VERSSDGQITQIIYKGQHDHERPQNRRGGGGRDSTEVGGAGQMMESSDDSGYRKDHDDDD
DDDEDDEDLPASKIRRIDGVSTTHRTVTEPKIIVQTKSEVDLLDDGYRWRKYGQKVVKGN
PHPRSYYKCTTPNCTVRKHVERASTDAKAVITTYEGKHNHDVPAARNGTAAATAAAVGPS
DHHRMRSMSGNNMQQHMSFGNNNNTGQSPVLLRLKEEKITI*
>G2059 (58..1089)
TTAAGAACAGGCTTCATTCTCTGGACAAACACTCAAAAAACAAACAAAAAAAGGAACATG
GAAGATCAGTTTCCTAAAATAGAAACTAGCTTCATGCACGACAAGCTCTTGTCTTCTGGA
ATCTACGGGTTCTTGAGTTCTTCGACGCCGCCACAACTTCTCGGTGTTCCAATATTTTTG
GAAGGTATGAAATCTCCTCTTCTTCCTGCTTCTTCGACTCCGAGCTACTTTGTGTCGCCT
CATGATCATGAGCTCACATCTTCTATTCATCCATCTCCGGTAGCTTCTGTTCCTTGGAAC
TTTCTAGAATCTTTTCCTCAGTCTCAACATCCTGATCATCATCCTTCTAAACCTCCAAAC
CTTACTTTGTTCCTTAAAGAACCAAAGCTACTAGAACTTTCTCAATCCGAAAGCAACATG
AGCCCTTACCATAAATACATCCCAAACTCCTTTTATCAATCAGACCAAAACAGAAACGAA
TGGGTAGAGATCAATAAAACTCTAACCAACTATCCCTCGAAAGGTTTTGGAAACTATTGG
CTAAGTACCACCAAGACTCAACCCATGAAGTCAAAAACAAGAAAGGTTGTTCAGACGACG
ACCCCAACAAAACTGTATAGAGGAGTGAGACAAAGACACTGGGGCAAATGGGTCGCAGAG
ATTAGGCTTCCAAGGAACAGAACCCGTGTTTGGCTCGGCACTTTTGAAACCGCTGAGCAA
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TTTCCTGATCTTAAACACCAGCTCAAGTCCGGTTCTTTGCGATGCATGATCGCCTCACTT
TTGGAGTCCAAGATTCAACAGATCTCATCTTCCCAAGTAAGTAACTCTCCTTCTCCTCCT
CCTCCAAAAGTGGGAACACCGGAGCAAAAGAATCATCACATGAAGATGGAGTCAGGAGAA
GACGTGATGATGAAGAAACAGAAAAGCCATAAGGAAGTGATGGAAGGAGATGGTGTACAA
TTGAGTAGGATGCCTTCTTTGGATATGGATCTCATTTGGGATGCTCTCTCATTTCCTCAT
TCTTCTTGACTTCAAATTAATATTTGTCAAACTTATTTTACTTACTTCTACCCTTTTTTA
TATCAAAAGTTTCCACCAAAGAAAGAAATTCATATTATGATGCCAAGATTGGTTTGCATT
TGGGGTTGAACACATTGTAATTCTTCTTACGACCACATAATCAAGTGGTTCTCCTTTTTT
TGTCTGCTAA
>G2059 Amino Acid Sequence (conserved domain in AA coordinates:184-254)
MEDQFPKIETSFMHDKLLSSGIYGFLSSSTPPQLLGVPIFLEGMKSPLLPASSTPSYFVS
PHDHELTSSIHPSPVASVPWNFLESFPQSQHPDHHPSKPPNLTLFLKEPKLLELSQSESN
MSPYHKYIPNSFYQSDQNRNEWVEINKTLTNYPSKGFGNYWLSTTKTQPMKSKTRKVVQT
TTPTKLYRGVRQRHWGKWVAEIRLPRNRTRVWLGTFETAEQAAMAYDTAAYILRGEFAHL
NFPDLKHQLKSGSLRCMIASLLESKIQQISSSQVSNSPSPPPPKVGTPEQKNHHMKMESG
EDVMMKKQKSHKEVMEGDGVQLSRMPSLDMDLIWDALSFPHSS*
>G2105 (42..1487)
CTCTCTGACTTGAACTCTTCTCTTCTACCGAATCAAACCAAATGGAGGATCATCAAAACC
ATCCACAGTACGGTATAGAACAACCATCTTCTCAATTCTCCTCTGATCTCTTCGGCTTCA
ACCTCGTTTCAGCGCCGGACCAGCACCATCGTCTTCATTTCACCGACCATGAGATAAGTT
TATTGCCACGTGGAATACAAGGGCTTACGGTGGCTGGAAACAACAGTAACACTATTACAA
CGATCCAGAGTGGTGGCTGTGTTGGTGGGTTTAGTGGCTTTACGGACGGCGGAGGAACAG
GGAGGTGGCCGAGGCAAGAGACGTTGATGTTGTTGGAGGTCAGATCTCGTCTTGATCACA
AGTTCAAAGAAGCTAATCAAAAGGGTCCTCTCTGGGATGAAGTTTCTAGGATTATGTCGG
AGGAACATGGATACACTAGGAGTGGCAAGAAGTGTAGAGAGAAGTTCGAGAATCTCTACA
AGTACTATAAAAAAACAAAAGAAGGCAAATCCGGTCGGCGACAAGATGGTAAAAACTATA
GATTTTTCCGGCAGCTTGAAGCGATATACGGCGAATCCAAAGACTCGGTTTCTTGCTATA
ACAACACGCAGTTCATAATGACCAATGCTCTTCATAGTAATTTCCGCGCTTCTAACATTC
ATAACATCGTCCCTCATCATCAGAATCCCTTGATGACCAATACCAATACTCAAAGTCAA
GCCTTAGCATTTCTAACAATTTCAACTCCTCCTCCGATTTGGATCTAACTTCTTCCTCTG
AAGGAAACGAAACTACTAAAAGAGAGGGGATGCATTGGAAGGAAAAGATCAAGGAATTCA

TTGGTGTTCATATGGAGAGGTTGATAGAGAAGCAAGATTTTTGGCTTGAGAAGTTGATGA
AGATTGTGGAAGACAAAGAACATCAAAGGATGCTGAGAGAAGAGGAATGGAGAAGGATTG
AAGCGGAAAGGATCGATAAGGAACGTTCGTTTTGGACAAAAGAGAGGGAGAGGATTGAAG
CTCGGGATGTTGCGGTGATTAATGCCTTGCAGTACTTGACGGGAAGGGCATTGATAAGGC
CGGATTCTTCGTCTCCTACAGAGAGGATTAATGGGAATGGAAGCGATAAAATGATGGCTG
ATAATGAATTTGCTGATGAAGGAAATAAGGGCAAGATGGATAAAAAACAAATGAATAAGA
AAAGGAAGGAGAAATGGTCAAGCCACGGAGGGAATCATCCAAGAACCAAAGAGAATATGA
TGATATACAACAATCAAGAAACTAAGATTAATGATTTTTGTCGAGATGATGACCAATGCC
ATCATGAAGGTTACTCACCTTCAAACTCCAAGAACGCAGGAACTCCGAGCTGCAGCAATG
CCATGGCAGCTAGTACAAAGTGCTTTCCATTGCTTGAAGGAGAAGGAGATCAGAACTTGT
GGGAGGGTTATGGTTTGAAGCAAAGGAAAGAAAATAATCATCAGTAAGCTACATTTTTCA
TTCTCAAAATGAAGAATAAGAGAACTTAGAAACGAT

>G2105 Amino Acid Sequence (domain in AA coordinates: 100-153)

MEDHQNHPQYGIEQPSSQFSSDLFGFNLVSAPDQHHRLHFTDHEISLLPRGIQGLTVAGN
NSNTITTIQSGGCVGGFSGFTDGGGTGRWPRQETLMLLEVRSRLDHKFKEANQKGPLWDE
VSRIMSEEHGYTRSGKKCREKFENLYKYYKKTKEGKSGRRQDGKNYRFFRQLEAIYGESK
DSVSCYNNTQFIMTNALHSNFRASNIHNIVPHHQNPLMTNTNTQSQSLSISNNFNSSSDL
DLTSSSEGNETTKREGMHWKEKIKEFIGVHMERLIEKQDFWLEKLMKIVEDKEHQRMLRE
EEWRRIEAERIDKERSFWTKERERIEARDVAVINALQYLTGRALIRPDSSSPTERINGNG
SDKMMADNEFADEGNKGKMDKKQMNKKRKEKWSSHGGNHPRTKENMMIYNNQETKINDFC
RDDDQCHHEGYSPSNSKNAGTPSCSNAMAASTKCFPLLEGEGDQNLWEGYGLKQRKENNH
Q*

>G2117 (49..465)

ATACTTGTCAACAAAAATTTTCTTAAAGAACGCATAACTGTTTTTTTCATGGCTGGTTCT
GTCTATAACCTTCCAAGTCAAAACCCTAATCCACAGTCTTTATTCCAAATCTTTGTTGAT
CGAGTACCACTTTCAAACTTGCCTGCCACGTCAGACGACTCTAGCCGGACTGCAGAAGAT
AATGAGAGGAAGCGGAGAAGGAAGGTATCGAACCGCGAGTCAGCTCGGAGATCGCGTATG
CGGAAACAGCGTCACATGGAAGAACTGTGGTCCATGCTTGTTCAACTCATCAATAAGAAC
AAATCTCTAGTCGATGAGCTAAGCCAAGCCAGGGAATGTTACGAGAAGGTTATAGAAGAG
AACATGAAACTTCGAGAGGAAAACTCCAAGTCGAGGAAGATGATTGGTGAGATCGGGCTT
AATAGGTTTCTTAGCGTAGAGGCCGATCAGATCTGGACCTTCTAATCGTCTCGTAAGCTT
GTTGGTTTTTGTTGTTTATTTAAAG

>G2117 Amino Acid Sequence (conserved domain in AA coordinates:46-106)

MAGSVYNLPSQNPNPQSLFQIFVDRVPLSNLPATSDDSSRTAEDNERKRRRKVSNRESAR
RSRMRKQRHMEELWSMLVQLINKNKSLVDELSQARECYEKVIEENMKLREENSKSRKMIG
EIGLNRFLSVEADQIWTF*

>G2124 (87..923)

GAACAGCAAAACCCTAGATTTCCTGTTCAAGCTCAAGACCGTACAAAACTTTGGAACTCA
TATATAAAGATCTCGAGAATAGCATTATGAATATCGTCTCTTGGAAAGATGCAAACGACG
AAGTTGCAGGCGGCGCTACGACAAGACGTGAAAGAGAAGTAAAAGAGGATCAAGAAGAAA
CCGAAGTCAGAGCCACCAGTGGCAAAACCGTAATTAAAAAGCAGCCTACATCGATCTCTT
CTTCTTCTTCTTCGTGGATGAAATCCAAGGATCCGAGGATTGTTAGGGTTTCACGCGCCT
TTGGAGGCAAAGACCGTCACAGCAAAGTGTGTACGTTACGTGGACTACGTGACAGACGCG
TGAGATTATCAGTCCCAACGGCTATTCAGCTCTACGATCTTCAAGAACGGCTCGGTGTTG
ACCAGCCTAGCAAAGCCGTTGACTGGTTGCTTGATGCAGCTAAAGAGGAGATCGACGAGC
TACCTCCGTTACCTATCTCGCCGGAAAATTTCAGCATCTTCAACCATCATCAGTCCTTCT
TGAATCTTGGTCAACGGCCCGGTCAAGATCCGACCCAACTCGGGTTTAAAATCAATGGAT
GTGTACAAAAGTCTACTACTACTAGCCGCGAAGAAAACGATAGAGAGAAAGGAGAAAACG
ATGTCGTTTACACAAACAATCATCATGTTGGGTCTTATGGAACTTATCACAACCTGGAAC
ATCATCATCATCATCACCAACATTTGAGTTTACAGGCAGATTATCATAGTCATCAACTAC
ATAGTCTTGTCCCATTTCCATCACAAATTTTGGTATGTCCAATGACGACATCACCAACAA
CTACAACTATACAATCTTTGTTTCCATCATCATCGTCAGCTGGTTCAGGGACTATGGAGA
CATTAGATCCGAGGCAAATGTAGCAACAATGGTGGTAGAGACATTGATAATCGGATGTCG
TCGGTCCAATTCAACCGAACTAATAGCACTACAACGGCTAACATGTCGAGGCATCTAGGC
TCGGAGCGTTGTACAAGTAGAGGAAGTGATCACCATATGTGAAGTTAGATTATTGAAACG
ATATAATTGTTGTTTGATGTGTTCAGAAATAAGGGGACAC

>G2124 Amino Acid Sequence (domain in AA coordinates: 75-132)

MNIVSWKDANDEVAGGATTRREREVKEDQEETEVRATSGKTVIKKQPTSISSSSSSWMKS
KDPRIVRVSRAFGGKDRHSKVCTLRGLRDRRVRLSVPTAIQLYDLQERLGVDQPSKAVDW
LLDAAKEEIDELPPLPISPENFSIFNHHQSFLNLGQRPGQDPTQLGFKINGCVQKSTTTS
REENDREKGENDVVYTNNHHVGSYGTYHNLEHHHHHHQHLSLQADYHSHQLHSLVPFPSQ
ILVCPMTTSPTTTTIQSLFPSSSSAGSGTMETLDPRQM*
>G2140 (148..1254)
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CACATATATATATACATATATAGAGAGAGAGAAGAGGACAAAGAGTTGAAAGATGAAGAC
TCTCATGTCTTCATAGAAACAAGTGATATGTGCGCTAAGAAAGAAGAAGAAGAAGAAGAA
GAAGAAGACAGTTCTGAAGCCATGAACAACATACAAAATTACCAAAATGACCTCTTCTTT
CACCAACTCATCTCTCATCATCACCATCATCATCATGATCCTTCTCAATCTGAAACTTTG
GGAGCATCCGGTAACGTTGGATCTGGTTTCACTATCTTCTCTCAAGATTCCGTCTCTCCA
ATATGGTCTCTACCTCCACCTACCTCGATCCAACCACCATTTGATCAGTTTCCTCCTCCT
TCTTCTTCTCCAGCATCTTTCTACGGAAGTTTCTTCAACAGAAGTCGAGCTCATCATCAG
GGATTACAGTTTGGGTACGAGGGTTTTGGTGGAGCCACGTCAGCAGCACATCATCATCAT
GAACAACTTCGGATCTTGTCGGAAGCTTTAGGTCCGGTAGTACAAGCCGGGTCCGGTCCT
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CATCTCGCTAAGCTCCGTAGCATATTACCCAACACCACCAAAACGGATAAAGCGTCGTTA
CTAGCTGAAGTGATCCAACATGTGAAAGAGTTGAAGAGAGAGACTTCAGTGATCTCAGAG
ACAAATCTTGTCCCAACGGAAAGCGATGAGTTAACGGTAGCTTTCACGGAGGAGGAAGAA
ACCGGAGATGGCAGATTTGTAATTAAAGCGTCGCTTTGCTGTGAAGACAGGTCGGATCTC
TTGCCTGACATGATTAAAACATTGAAAGCTATGCGTCTCAAAACGCTCAAGGCGGAGATA
ACCACCGTTGGGGGACGAGTCAAGAACGTTTTGTTTGTTACCGGAGAAGAGAGCTCCGGT
GAGGAAGTGGAGGAAGAGTACTGTATAGGGACGATTGAGGAAGCTTTGAAAGCGGTGATG
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AGTCACAACACTATCACTATCGTCGAACAACAACAACAATATAATCAGAGGTAATCAATT
TTTTACTTAAATCGCTTTTTTTTCTTACTTTCGGTGTATCTACTACGTGTGTTGTTTGCT
GGTTATGGAAATGAATGTTGTACGTCACGTTATACTATAGATATATGTGTGTTTGTGTGT
ATGTATAACGGAAGTATTTGTATCCGTTGTGGTCTTGGACTTTTGGTTTGGTTCTAAGAT
ACTTATTTTTAAAAACTTGTATCGTTGAGTTGGTTTTCTAGATATGCTTAATGGGAGTAT
GTGACGAAAAAAAA
>G2140 Amino Acid Sequence (domain in AA coordinates:167-242)
MCAKKEEEEEEEEDSSEAMNNIQNYQNDLFFHQLISHHHHHHDPSQSETLGASGNVGSG
FTIFSQDSVSPIWSLPPPTSIQPPFDQFPPPSSSPASFYGSFFNRSRAHHQGLQFGYEGF
GGATSAAHHHHEQLRILSEALGPVVQAGSGPFGLQAELGKMTAQEIMDAKALAASKSHSE
AERRRRERINNHLAKLRSILPNTTKTDKASLLAEVIQHVKELKRETSVISETNLVPTESD
ELTVAFTEEEETGDGRFVIKASLCCEDRSDLLPDMIKTLKAMRLKTLKAEITTVGGRVKN
VLFVTGEESSGEEVEEEYCIGTIEEALKAVMEKSNVEESSSSGNAKRQRMSSHNTITIVE
QQQQYNQR*
>G2144 (102..1241)
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TTGGAGCTAGATCCGGCGGTGTTGGACCGTGCCGGGAACCAATAGGCCTTGAATCGCTAC
ATCTCGGTGACGAATTTCGGCAACTAGTGACGACTTTACCTCCCGAGAACCCCGGCGGTT
CGTTCACGGCTTTGCTTGAGCTTCCACCTACACAAGCAGTGGAGCTTCTCCATTTCACTG
ATTCTTCGTCTTCTCAACAAGCGGCAGTGACAGGGATCGGTGGAGAGATTCCTCCGCCGC
TTCACTCTTTCGGTGGGACATTGGCTTTTCCTTCTAACTCAGTTCTCATGGAGCGAGCAG
CTCGTTTCTCGGTGATTGCCACTGAGCAACAAAACGGAAATATCTCCGGGGAGACTCCGA
CGAGCTCTGTACCTTCCAATTCAAGTGCTAATCTCGACAGAGTCAAGACGGAGCCTGCTG
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CTAACCAGAACAATCGAAATGGGAAGAGGAAAGATTTCGAAAAGAAGGGTAAAAGCTCGA
CGAAGAAGAACAAAAGCTCTGAAGAGAACGAGAAGCTGCCATATGTTCACGTTAGAGCTC
GTCGTGGTCAAGCAACCGATAGCCATAGCTTAGCAGAACGAGCAAGAAGAGAGAAGATAA
ATGCACGAATGAAGCTGTTACAGGAACTGGTCCCAGGCTGTGATAAGATTCAAGGTACCG
CGCTGGTGCTGGATGAAATCATTAACCATGTCCAGTCATTACAACGTCAAGTGGAGATGC
TATCAATGAGACTTGCTGCGGTAAACCCCAGAATCGACTTCAATCTCGACACCATATTGG

CTTCAGAAAACGGTTCTTTAATGGATGGGAGCTTCAATGCCGCACCAATGCAGCTTGCTT
GGCCTCAGCAAGCCATTGAGACCGAACAGTCCTTTCATCACCGGCAACTGCAACAACCAC
CAACACAACAATGGCCTTTTGACGGCTTGAACCAGCCGGTATGGGGAAGAGAAGAGGATC
AAGCTCATGGCAATGATAACAGCAATTTGATGGCAGTTTCTGAAAATGTAATGGTGGCTT
CTGCTAATTTGCACCCAAATCAGGTCAAAATGGAGCTGTAAGTTGGGAAAACGGTAGAGA
TCATGAATGTGTATATACATCGTATAAGCTCGTTTCTCTCTATATAAATATAATCATAAA
TATAGATATCTGTTAAGAAGGTATCAGTCATTTGATTCAGAGAGACAACACTGGTATGAT
TGTTTCTTATTCTTGTACCAGATTTCGACAATGTAGAATTTAGTAGGATATGATCATTTT
GATCTCGTTATATATA
>G2144 Amino Acid Sequence (domain in AA coordinates:203-283)
MDLTGGFGARSGGVGPCREPIGLESLHLGDEFRQLVTTLPPENPGGSFTALLELPPTQAV
ELLHFTDSSSSQQAAVTGIGGEIPPPLHSFGGTLAFPSNSVLMERAARFSVIATEQQNGN
ISGETPTSSVPSNSSANLDRVKTEPAETDSSQRLISDSAIENQIPCPNQNNRNGKRKDFE
KKGKSSTKKNKSSEENEKLPYVHVRARRGQATDSHSLAERARREKINARMKLLQELVPGC
DKIQGTALVLDEIINHVQSLQRQVEMLSMRLAAVNPRIDFNLDTILASENGSLMDGSFNA
APMQLAWPQQAIETEQSFHHRQLQQPPTQQWPFDGLNQPVWGREEDQAHGNDNSNLMAVS
ENVMVASANLHPNQVKMEL*
>G2431 (47..1057)
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GAGCCTTGTGTTGTCAACGGATGCTAAGCCAAGGTTGAAATGGACTTGTGATCTTCATCA
CAAATTCATCGAAGCCGTTAATCAACTTGGAGGACCTAACAAAGCAACACCTAAGGGTTT
GATGAAGGTTATGGAGATTCCTGGGCTTACCTTATACCATCTCAAGAGCCATTTACAGAA
ATATCGGTTAGGGAAGAGCATGAAGTTCGATGATAACAAGCTAGAAGTTTCCTCTGCATC
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GATGGAAGTTCAGAAGAAACTTCATGAACAAATCGAAGTTCAGAGGCATTTGCAGGTGAA
GATTGAGGCACAAGGAAAGTATCTACAGTCCGTTTTAATGAAAGCTCAACAAACTCTCGC
TGGCTACTCATCTTCAAATCTCGGCATGGATTTTGCGAGGACCGAGCTCTCTAGATTAGC
TTCAATGGTGAACAGAGGCTGTCCAAGCACTTCGTTCTCAGAGCTAACGCAAGTAGAAGA
AGAAGAAGAAGGTTTCTTGTGGTACAAGAAACCAGAAAACAGAGGAATTAGTCAGCTGAG
ATGTTCAGTAGAGAGCTCGTTGACATCTTCAGAGACCTCAGAGACAAAACTGGATACTGA
CAATAACCTTAATAAATCGATTGAACTTCCGTTGATGGAGATCAACTCGGAAGTGATGAA
GGGGAAGAAGAGAAGCATAAACGACGTCGTTTGCGTGGAGCAGCCTCTAATGAAGAGAGC
TTTTGGAGTTGATGATGATGAGCATTTGAAGTTGAGTTTGAATACTTACAAGAAAGACAT
GGAGGCGTGTACGAACATAGGACTAGGGTTTAATTAAAAAAAAAACATTTTACTAAAGTT
ATATAAAAATGTTTTAAAAGAATCCA
>G2431 Amino Acid Sequence (conserved domain in AA coordinates:38-88)
MCLLMEINNNANNTNTTIDNHKAKMSLVLSTDAKPRLKWTCDLHHKFIEAVNQLGGPNKA
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>G2465 (86..1150)
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>G2465 Amino Acid Sequence (conserved domain in AA coordinates:219-269)
MMVEMDYAKKMQKCHEYVEALEEEQKKIQVFQRELPLCLELVTQAIEACRKELSGTTTTT
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>G2583 (38..607)
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>G2583 Amino Acid Sequence (domain in AA coordinates:4-71)
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>G2724 (1..651)
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>G2724 Amino Acid Sequence (conserved domain in AA coordinates:7-113)
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>G377 (1..396)
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>G377 Amino Acid Sequence (domain in AA coordinates:85-128)
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HTTCPLCRSIL*
>G428 (97..1032)
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>G428 Amino Acid Sequence (domain in AA coordinates: 229-292)
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DDSNETFFTEE*
>G447 (241..3501)
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>G447 Amino Acid Sequence (conserved domain in AA coordinates:22-356)

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AASFNR*
>G464 (41..760)
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>G464 Amino Acid Sequence (domain in AA coordinates: 20-28, 71-82, 126-142, 187-224)
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SDFVLTYEDKEGDWMLVGDVPWRMFINSVKRLRIMGTSEASGLAPRRQEQKDRQRNNPV*
>G557 (192..698)
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>G557 Amino Acid Sequence (domain in AA coordinates: 90-150)
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>G577 (44..2155)
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>G674 (1..786)—
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>G804 Amino Acid Sequence (domain in AA coordinates: 54-117)
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TGTTAGCATCGTCTGGTGCACAGCCTACTCTGTTCCAGAAACGTGCAGCTATGCGTCAGA
GCTCTGGAAGCAAAATGGGAAATTCGGAGAGTTCGGGAATGAGGAGGTTTAGTGATGATG
GAGATATGGATGAGACTGGGATTGAGGTTTCTGGGTTGAACTATGAGTCTGATGAGATAA
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AAGGTATGCCTGCTAAGAATCTGATGGCTGAGAGGAGAAGGAGGAAGAAGCTTAATGATA
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CACCTACACCGCAAACTCTTTCTTGTCGTGTCAAGGAAGAGTTGTGTCCCTCTTCTTTAC
CAAGTCCTAAAGGCCAGCAAGCTAGAGTTGAGGTTAGATTAAGGGAAGGAAGAGCAGTGA
ACATTCATATGTTCTGTGGTCGTAGACCGGGTCTGTTGCTCGCTACCATGAAAGCTTTGG
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ATGTTTTCCGCGCTGAGCAATGCCAAGAAGGACAAGAGATACTGCCTGATCAAATCAAAG
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CCATTAAGCATCTGTTGAAGCAGAGCTAGAAGAACTAAGTCCCTTTAAATCTGCAATTTT
CTTCTCAACTTTTTTTCTTATGTCATAACTTCAATCTAAGCATGTAATGCAATTGCAAAT

GAGAGTTGTTTTTAAATTAAGCTTTTGAGAACTTGAGGTTGTTGTTGTTGGATACATAAC
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>G1062 Amino Acid Sequence (domain in AA coordinates: 308-359)
MGLDGNNGGGVWLNGGGGEREENEEGSWGRNQEDGSSQFKPMLEGDWFSSNQPHPQDLQM
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NVPSSANPFDNAFEFGSESGFLNQIHAPISMGFGSLTQLGNRDLSSVPDFLSARSLLAPE
SNNNNTMLCGGFTAPLELEGFGSPANGGFVGNRAKVLKPLEVLASSGAQPTLFQKRAAMR
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KKGMPAKNLMAERRRRKKLNDRLYMLRSVVPKISKMDRASILGDAIDYLKELLQRINDLH
NELESTPPGSLPPTSSSFHPLTPTPQTLSCRVKEELCPSSLPSPKGQQARVEVRLREGRA
VNIHMFCGRRPGLLLATMKALDNLGLDVQQAVISCFNGFALDVFRAEQCQEGQEILPDQI
KAVLFDTAGYAGMI*
>G1322 (213..833)
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CCCGCCTCGAGTATCTCTCTCTCTCTCTCTCTTCTCTGTTTTCTTTATTGATTGCATAGA
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GGAACTCTGTCGCCAAAGCCTCTGGTCTAAAACGTACTGGAAAAAGTTGTCGGCTCCGGT
GGCTGAACTATCTCCGACCAGATGTGCGGCGAGGGAACATAACCGAAGAAGAACAGCTTT
TGATCATTCAGCTTCATGCTAAGCTTGGAAACAGGTGGTCGAAGATTGCGAAGCATCTTC
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>G1322 Amino Acid Sequence (domain in AA coordinates:26-130)
METTMKKKGRVKATITSQKEEEGTVRKGPWTMEEDFILFNYILNHGEGLWNSVAKASGLK
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WRTKIQRHMKVSSENMMNHQHHCSGNSQSSGMTTQGSSGKAIDTAESFSQAKTTTFNVVE
QQSNENYWNVEDLWPVHLLNGDHHVI*
>G1331 (1..786)
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AGAGGACAGATCACTCCACATGAAGAAAGTATAATACTTGAGCTACACGCTAAGTGGGGA
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GAAAACAATAGCAGTAGCAGTAGCGATGGCGGTGGTGATGTGTTCTATTATCCTGATCAA
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GGTAGATTTTCTCCTGTAAACATACCTGATGCTAATACTATGAACGAAGACAATGCCATA
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TGTTAA
>G1331 Amino Acid Sequence (conserved domain in AA coordinates:8-109)
MVEEVWRKGPWTAEEDRLLIEYVRVHGEGRWNSVSKLAGLKRNGKSCRLRWVNYLRPDLK
RGQITPHEESIILELHAKWGNRWSTIARSLPGRTDNEIKNYWRTHFKKKAKPTTNNAEKI
KSRLLKRQHFKEQREIELQQEQQLFQFDQLGMKKIISLLEENNSSSSSDGGGDVFYYPDQ
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AATAACGPRKPYFHNLVIPFC*
>G1521 (1..891)

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GAGCAATTACCAATTCTTCGTGATCGTGAGACTTTAACTTATCATCGGAATAATCCTTCC
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AGGCCATTGCCATGGCGGAGATCATTTGGACGACCAGGTTCAGTTCCTGATTCTGTTATC
TTCCAGCGAAAGCTTCAGTGGCGAGCTAGCATATACACTAAGCAATTACGAGCTGTTCGA
TTACATTCAAGGCGCTTGGAACTAAGTTTGGCGGTGAATGATTACACCAAAGCAAAGATA
ACTGAAAGAATTGAGCCATGGATTAGAAGAGAGCTTCAGGCAGTCCTTGGAGATCCTGAT
CCCTCAGTTATTGTTCATTTTGCGTCAGCTCTTTTCATCAAAAGGCTTGAGAGAGAGAAT
AATCGACAAACCGGGCAGACCGGGATGTTGGTGGAAGATGAAGTCTCCTCTCTTCGAAAA
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>G1521 Amino Acid Sequence (domain in AA coordinates: 39-80)

MPPLPSSTAPSSSRHLRSPESIAKFAGRAIFPALQGKSCPICLENLTERRSAAVITVCKH
GYCLACIRKWSSFKRNCPLCNTRFDSWFIVSDFASRKYHKEQLPILRDRETLTYHRNNPS
DRRRIIQRSRDVLENSSSRSRPLPWRRSFGRPGSVPDSVIFQRKLQWRASIYTKQLRAVR
LHSRRLELSLAVNDYTKAKITERIEPWIRRELQAVLGDPDPSVIVHFASALFIKRLEREN
NRQTGQTGMLVEDEVSSLRKFLSDKVDIFWHELRCFAESILTMETYDAVVEYNEVE*

>G183 (1..1458)

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GAAGAAAACATGAGTCCTTTGGATGCATTTTTCAGGAGCTCGAATGTTCCTAATTCTCCT
GTCGTTGCAATCTCTCCAGGATTCAGTCCATCAGCACTATTGCATACTCCCAATATGGTC
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GGGGCAACAATACCTCAAAATCAGAATGATCGAACCAGTCGGTTAGGTAGGGCTCCTCCT
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TCTTCGTTGGCTACAGAAATTGATCTGACAGAGGTTTATATGACCGGAATCTCTATGCTG
CCGAATATACCGGTTTACGAGAATTCGGGTTTTATGTACCAGAATGATGAACCGACGATG
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TTTGGTGTCGACATGTAG

>G183 Amino Acid Sequence (domain in AA coordinates: TBD)

MSDFDENFIEMTSYWAPPSSPSPRTILAMLEQTDNGLNPISEIFPQESLPRDHTDQSGQR
SGLRERLAARVGFNLPTLNTEENMSPLDAFFRSSNVPNSPVVAISPGFSPSALLHTPNMV
SDSSQIIPPSSATNYGPLEMVETSGEDNAAMMMFNNDLPYQPYNVDLPSLEVFDDIATEE
SFYIPSYEPHVDPIGTPLVTSFESELVDDAHTDIISIEDSESEDGNKDDDEDFQYEDED
EDQYDQDQDVDEDEEEEKDEDNVALDDPQPPPPKRRYEVSNMIGATRTSKTQRIILQME
SDEDNPNDGYRWRKYGQKVVKGNPNPRSYFKCTNIECRVKKHVERGADNIKLVVTTYDGI
HNHPSPPARRSNSSSRNRSAGATIPQNQNDRTSRLGRAPPTPTPPTPPPSSYTPEEMRPF
SSLATEIDLTEVYMTGISMLPNIPVYENSGFMYQNDEPTMNAMPDGSDVYDGIMERLYFK
FGVDM*

>G2555 (177..956)
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AATCCACTCATATAAGCGGCGGAAGTAGCGGTGGTGGTGGTGGAGGAGGAGGAGAGGTGA
GTCGAAGTGGATTATCTCGGATCCGTTCAGCTCCAGCTACTTGGATTGAAACCCTACTCG
AAGAAGATGAAGAAGAAGGTTTAAAACCTAACCTTTGTTTAACAGAGCTGCTTACTGGTA
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TGTTCGAAAATTCGAAACATGATCTTATATATTGAACTAGAAAAAATAGATATATATGAA
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>G2555 Amino Acid Sequence (domain in AA coordinates: 175-245)
MQSTHISGGSSGGGGGGGGEVSRSGLSRIRSAPATWIETLLEEDEEEGLKPNLCLTELLT
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GIPANYDYLSTNVDISPTKRSRDMETQFSSQLKEEQMSGGISGMMDMNMDKIFEDSVPCR
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IQELTEQQKRCKCKPKEEQ*
>G375 (53..1171)
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>G375 Amino Acid Sequence (domain in AA coordinates: 75-103)
MGLTSLQVCMDSDWLQESESSGGSMLDSSTNSPSAADILAACSTRPQASAVAVAAAALMD
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HHMGLNHGVGLNNNNNNGGFNGISTGGNGNGGGLMDISTCQRLMLSNYDHHHYNHQEDHQ
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GYGTSTKTNSLV*
>G1007 (86..763)
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GAGCTGGGGGAAATGGGTCTCGGAGATTCGGGAGCCCCGTAAGAAATCAAGAATCTGGCT
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AAAAAAAAAAAAAAAAAAAAAA
>G1007 Amino Acid Sequence (domain in AA coordinates: TBD)
MVDSHGSDTECSSKKKKEKTKEKGVYRGARMRSWGKWVSEIREPRKKSRIWLGTFPTAEM
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>G1010 (344..1276)
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>G1010 Amino Acid Sequence (domain in AA coordinates: 33-122)
MMTDLSLTRDEDEEEAKPLAEEEGAREVADREHMFDKVVTPSDVGKLNRLVIPKQHAERF
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KSSLSFDLDQ*
>G1014 (174..1112)
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CTTCCACACTTCCTTTTTACTAGGCAGTGTTAACCAATTGAGAGAGAAAAATGATGGTTG
ATGAAAATGTGGAAACCAAGGCCTCTACTTTAGTGGCAAGTGTTGATCATGGGTTTGGAT
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>G1014 Amino Acid Sequence (domain in AA coordinates: 90-172)
MVDENVETKASTLVASVDHGFGSGSGHDHHGLSASVPLLGVNWKKRRMPRQRRSSSSFNL
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YSNNYVIQARKASEEEEVDVINLEEDDVYTNLTRIENTVVNDLLLQDFNHHNNNNNNNSN
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GSVENISLDDFY*
>G1035 (103..624)
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CTTGAACTTAACCACCGTCTCCAATCTCTTAACGAGATCGTTGATTTCGTCGAATCTTCT
TCTTCAGGATTCGGTATGGAGACCGGTCAGGGATTATTCGACGGTGGATTATTCGACGGC
GTGATGAATCCTATGAATCTAGGGTTTTATAATCAACCAATCATGGCTTCTGCTTCTACT
GCTGGTGATGTTTTCAACTGTTAGAAAACTTCACATCATTATCATCGTGAGTGAGACTAA
TCATCGCAGCAGGGGTAAAACTGTAATTTTTCTTATAAATTATGTGATGATGCTTTGTTT
CTTTATTTTATAAGATGGTTAATTAGTGTTTAAAACTGATTGTAATGATAGACAGTGTAA
GAAATGTGTGATATCATGGAGATGGTGATGTGAGTTTGGTACAAATATTTTAAGATCTTT
TCTTTCTATATATTAAAAGTGAAGAAATAATATTTTGTCATTTTCTTAAAAAAAAAAAAA
AAA
>G1035 Amino Acid Sequence (domain in AA coordinates: 39-91)
MNNKTEMGSSTSGNCSSVSTTGLANSGSESDLRQRDLIDERKRKRKQSNRESARRSRMRK
QKHLDDLTAQVTHLRKENAQIVAGIAVTTQHYVTIEAENDILRAQVLELNHRLQSLNEIV
DFVESSSSGFGMETGQGLFDGGLFDGVMNPMNLGFYNQPIMASASTAGDVFNC*
>G1046 (1..567)
ATGATTAGACATCTAAAACCCTACATGGAGTCGTCTAGTGTCCATCGCTCTCATTGTTTC
GATATTCTTGATGGAGTCCCACTACACGACGATCATTTCAACTCGGCATTCCTACCAAAC
ACTGACTTTAATGTTCATTTGCAGTCAAACGTATCGACCCGCATCAACAATCAGTCTCAC
TTAGACCCAAATGCAGAAAACATTTTCCATAACGAAGGTCTTGCTCCAGAAGAAAGAAGA
GCAAGAAGAATGGTCTCTAACCGGGAATCTGCAAGGAGGTCACGTATGCGCAAAAAGAAG
CAGATCGAAGAGCTGCAACAACAAGTTGAACAACTCATGATGTTGAATCATCACTTGTCT
GAGAAAGTCATCAACTTGTTGGAAAGCAACCATCAGATCCTACAAGAGAACTCACAGCTG
AAAGAGAAAGTCTCTTCCTTTCACTTGCTCATGGCAGATGTGCTATTACCCATGAGAAAT
GCAGAGAGCAACATCAATGACCGCAATGTGAATTATCTAAGAGGAGAACCATCAAACCGT

CCCACCAACAGTCCCTTTGGTAAGTAA
>G1046 Amino Acid Sequence (conserved domain in AA coordinates:79-138)
MIRHLKPYMESSSVHRSHCFDILDGVPLHDDHFNSAFLPNTDFNVHLQSNVSTRINNQSH
LDPNAENIFHNEGLAPEERRARRMVSNRESARRSRMRKKKQIEELQQQVEQLMMLNHHLS
EKVINLLESNHQILQENSQLKEKVSSFHLLMADVLLPMRNAESNINDRNVNYLRGEPSNR
PTNSPFGK*
>G1049 (29..550)
CTAACTTTCTTCCCAAGTAAACTTCAAAATGCAGCCGCAAACAGACGTTTTCAGCCTCCA
TAACTACCTAAACTCATCGATACTGCAGTCTCCGTATCCTTCTAATTTCCCGATATCTAC
GCCATTTCCAACCAACGGTCAAAACCCGTACCTCCTCTACGGATTCCAAAGCCCTACAAA
CAATCCACAATCCATGAGCCTAAGCAGCAACAACTCAACATCAGATGAAGCAGAAGAGCA
GCAGACGAACAACAATATAATCAACGAGCGGAAGCAGAGAAGGATGATTTCAAACCGAGA
ATCCGCAAGGAGATCGCGTATGAGGAAGCAAAGACACCTTGACGAGCTTTGGTCACAAGT
GATGTGGTTAAGGATCGAGAATCATCAGTTGCTTGATAAGCTTAACAATCTCTCTGAGTC
TCACGACAAGGTTCTTCAAGAGAATGCTCAGCTTAAAGAAGAAACATTTGAGCTTAAGCA
AGTGATCAGCGATATGCAAATTCAAAGCCCTTTCTCTTGCTTTAGAGACGATATAATCCC
CATTGAATAAAGCATTTTTCCCCGATTCATATTTATGAAAATTTTCTTCAAGAGTATGTT
TCTTTGTATGTATATGTGGAGATGTATTTCAGGGTTTTGATAATATGACCCTTTACGACG
ACGTTTTTAGATTGTAGTAAATTTATAAACTAAAGAAGATTAGTGTTAATGAAGAACAAA
TATAA
>G1049 Amino Acid Sequence (domain in AA coordinates 77-132)
MQPQTDVFSLHNYLNSSILQSPYPSNFPISTPFPTNGQNPYLLYGFQSPTNNPQSMSLSS
NNSTSDEAEEQQTNNNIINERKQRRMISNRESARRSRMRKQRHLDELWSQVMWLRIENHQ
LLDKLNNLSESHDKVLQENAQLKEETFELKQVISDMQIQSPFSCFRDDIIPIE*
>G1069 (89..934)
TTGGAACCCTAGAGGCCTTTCAAGCAAATCATCAGGGTAACAATTTCTTGATCTTTCTTT
TTAGCGAATTTCCAGTTTTTGGTCAATCATGGCAAACCCTTGGTGGACGAACCAGAGTGG
TTTAGCGGGCATGGTGGACCATTCGGTCTCCTCAGGCCATCACCAAAACCATCACCACCA
AAGTCTTCTTACCAAAGGAGATCTTGGAATAGCCATGAATCAGAGCCAAGACAACGACCA
AGACGAAGAAGATGATCCTAGAGAAGGAGCCGTTGAGGTGGTCAACCGTAGACCAAGAGG
TAGACCACCAGGATCCAAAAACAAACCCAAAGCTCCAATCTTTGTGACAAGAGACAGCCC
CAACGCACTCCGTAGCCATGTCTTGGAGATCTCCGACGGCAGTGACGTCGCCGACACAAT
CGCTCACTTCTCAAGACGCAGGCAACGCGGCGTTTGCGTTCTCAGCGGGACAGGCTCAGT
CGCTAACGTCACCCTCCGCCAAGCCGCCGCACCAGGAGGTGTGGTCTCTCTCCAAGGCAG
GTTTGAAATCTTATCTTTAACCGGTGCTTTCCTCCCTGGACCTTCCCCACCCGGGTCAAC
CGGTTTAACGGTTTACTTAGCCGGGGTCCAGGGTCAGGTCGTTGGAGGTAGCGTTGTAGG
CCCACTCTTAGCCATAGGGTCGGTCATGGTGATTGCTGCTACTTTCTCTAACGCTACTTA
TGAGAGATTGCCCATGGAAGAAGAGGAAGACGGTGGCGGCTCAAGACAGATTCACGGAGG
CGGTGACTCACCGCCCAGAATCGGTAGTAACCTGCCTGATCTATCAGGGATGGCCGGGCC
AGGCTACAATATGCCGCCGCATCTGATTCCAAATGGGGCTGGTCAGCTAGGGCACGAACC
ATATACATGGGTCCACGCAAGACCACCTTACTGACTCAGTGAGCCATTTCTATATATAAT
GGTCTATATAAATAAATATATAGATGAATATAAGCAAGCAATTTGAGGTAGTCTATTACA
AAGCTTTTGCTCTGGTTGGAAAAATAAATAAGTATCAAAGCTTTGTTTGTTCTTAATGGA
AATATAGAGCTTGGGAAGGTAGAAAGAGACGACATT
>G1069 Amino Acid Sequence (domain in AA coordinates: 67-74)
MANPWWTNQSGLAGMVDHSVSSGHHQNHHHQSLLTKGDLGIAMNQSQDNDQDEEDDPREG
AVEVVNRRPRGRPPGSKNKPKAPIFVTRDSPNALRSHVLEISDGSDVADTIAHFSRRRQR
GVCVLSGTGSVANVTLRQAAAPGGVVSLQGRFEILSLTGAFLPGPSPPGSTGLTVYLAGV
QGQVVGGSVVGPLLAIGSVMVIAATFSNATYERLPMEEEEDGGGSRQIHGGGDSPPRIGS
NLPDLSGMAGPGYNMPPHLIPNGAGQLGHEPYTWVHARPPY*
>G1070 (170..1144)
TCGACCAGCTTGGATTTCGTTGTTCATCATTACTACTCTCTTTCTTCTTCTAGCTAGCTA
GTTTTGACAGCAAAATAAGAAGCAAAAAAAAGGTCAACTAAAAAAGATCTGTTCTTAGAT
CACTCTCTTCTTCTTTTTTTGATCCAATTCCACCATTGAATCATAGATCATGGATCCAGT
ACAATCTCATGGATCACAAAGCTCTCTACCTCCTCCTTTCCACGCAAGAGACTTTCAATT
ACATCTTCAACAACAGCAACAAGAGTTCTTCCTCCACCATCACCAGCAACAAAGAAACCA
AACCGATGGTGACCAACAAGGAGGATCAGGAGGAAACCGACAAATCAAGATGGATCGTGA

AGAGACAAGCGACAACATAGACAACATAGCTAACAACAGCGGTAGTGAAGGTAAAGACAT
AGATATACACGGTGGTTCAGGAGAAGGAGGTGGTGGCTCCGGAGGAGATCATCAGATGAC
AAGAAGACCAAGAGGAAGACCAGCGGGATCCAAGAACAAACCAAAACCACCGATTATCAT
CACACGGGACAGCGCAAACGCGCTTAGAACCCACGTGATGGAGATCGGAGATGGCTGCGA
CTTAGTCGAAAGCGTTGCCACTTTTGCACGAAGACGCCAACGCGGCGTTTGCGTTATGAG
CGGTACTGGAAATGTTACTAACGTCACTATACGTCAGCCTGGATCTCATCCTTCTCCTGG
CTCGGTAGTTAGTCTTCACGGAAGGTTCGAGATTCTATCTCTCTCAGGATCTTTTCTCCC
TCCTCCGGCTCCTCCTACAGCCACCGGATTGAGTGTTTACCTCGCTGGAGGACAAGGACA
GGTGGTTGGAGGAAGCGTAGTTGGTCCGTTGTTATGTGCTGGTCCTGTCGTTGTCATGGC
TGCGTCTTTTAGCAATGCGGCGTACGAAAGGTTGCCTTTAGAGGAAGATGAGATGCAGAC
GCCGGTTCATGGCGGAGGAGGAGGAGGATCATTGGAGTCGCCGCCAATGATGGGACAACA
ACTGCAACATCAGCAACAAGCTATGTCAGGTCATCAAGGGTTACCACCTAATCTTCTTGG
TTCGGTTCAGTTGCAGCAGCAACATGATCAGTCTTATTGGTCAACGGGACGACCACCGTA
TTGATCAAATATACACACACACTCATAATCGTTGCTAGCTAGCTAACGATGAATCATGAG
TTTAGTGGATATATATATGATTAAAAGAGGTTAGCTTATGAACATTAATAAGAGTTTGGA
TTCTATCGAGCTTCATTATGTTTGGGTCATCGTTC

>G1070 Amino Acid Sequence (domain in AA coordinates: 98-120)

MDPVQSHGSQSSLPPPFHARDFQLHLQQQQQEFFLHHHQQQRNQTDGDQQGGSGGNRQIK
MDREETSDNIDNIANNSGSEGKDIDIHGGSGEGGGGSGGDHQMTRRPRGRPAGSKNKPKP
PIIITRDSANALRTHVMEIGDGCDLVESVATFARRRQRGVCVMSGTGNVTNVTIRQPGSH
PSPGSVVSLHGRFEILSLSGSFLPPPAPPTATGLSVYLAGGQGQVVGGSVVGPLLCAGPV
VVMAASFSNAAYERLPLEEDEMQTPVHGGGGGGSLESPPMMGQQLQHQQQAMSGHQGLPP
NLLGSVQLQQQHDQSYWSTGRPPY*

>G1076 (198..1076)

ATTTTAGTCTTCCTATAACTTCTTCTCAATCCTCTCTCATATCTTTTTTCTTAGTTTAAA
TTTCAATAAAATAGAAAAAAAACATATACAAATCTACAGAGAAGAGAAGCTTTATTTTAAT
CTTGTGTGTGTGTGTGTGTTTTATATAATTTTTATTTTTTTTCAAATTAAAATCTCTTCT
TTGCTTTTGATGTGGGCATGGCTGGTCTTGATCTAGGCACAGCTTTTCGTTACGTTAATC
ACCAGCTCCATCGTCCCGATCTCCACCTTCACCACAATTCCTCCTCCGATGACGTCACTC
CCGGAGCCGGGATGGGTCATTTCACCGTCGACGACGAAGACAACAACAACAACCATCAAG
GTCTTGACTTAGCCTCTGGTGGAGGATCAGGAAGCTCTGGAGGAGGAGGAGGTCACGGCG
GGGGAGGAGACGTCGTTGGTCGTCGTCCACGTGGCAGACCACCGGGATCCAAGAACAAAC
CGAAACCTCCGGTAATTATCACGCGCGAGAGCGCAAACACTCTAAGAGCTCACATTCTTG
AAGTAACAAACGGCTGCGATGTTTTCGACTGCGTTGCGACTTATGCTCGTCGGAGACAGC
GAGGGATCTGCGTTCTGAGCGGTAGCGGAACGGTCACGAACGTCAGCATACGTCAGCCAT
CTGCGGCTGGAGCGGTTGTGACGCTACAAGGAACGTTCGAGATTCTTTCTCTCTCCGGAT
CGTTTCTTCCTCCTCCGGCACCTCCCGGAGCAACGAGTTTGACAATTTTCTTAGCCGGAG
GACAAGGTCAGGTGGTTGGAGGAAGCGTTGTGGGTGAGCTTACGGCGGCTGGACCGGTGA
TTGTGATTGCAGCTTCGTTTACTAATGTTGCTTATGAGAGACTTCCTTTAGAAGAAGATG
AGCAGCAGCAACAGCTTGGAGGAGGATCTAACGGCGGAGGTAATTTGTTTCCGGAGGTGG
CAGCTGGAGGAGGAGGAGGACTTCCGTTCTTTAATTTACCGATGAATATGCAACCAAATG
TGCAACTTCCGGTGGAAGGTTGGCCGGGGAATTCCGGTGGAAGAGGTCCTTTCTGATGTG
TATATATTGATAATCATTATATATATACCGGCGGAGAAGCTTTTCCGGCGAAGAATTTGC
GAGAGTGAAGAAAGGTTAGAAAAGCTTTTAATGGACTAATGAATTTCAAATTATCATCGT
GATTTCGGACATTGTCTTGTTCATCATGTTAAGCTTAGGTTTATTTTTTGTCGTTTGTAG
AATTTTATGTTTGAATCCTTTTTTTTTCTGTGAAACTCTATTGTGTTCGTCTGCGAAGG
AAAAAAAAATTCTCAAAAAAAA

>G1076 Amino Acid Sequence (domain in AA coordinates: 82-89)

MAGLDLGTAFRYVNHQLHRPDLHLHHNSSSDDVTPGAGMGHFTVDDEDNNNNHQGLDLAS
GGGSGSSGGGGGHGGGGDVVGRRPRGRPPGSKNKPKPPVIITRESANTLRAHILEVTNGC
DVFDCVATYARRRQRGICVLSGSGTVTNVSIRQPSAAGAVVTLQGTFEILSLSGSFLPPP
APPGATSLTIFLAGGQGQVVGGSVVGELTAAGPVIVIAASFTNVAYERLPLEEDEQQQQL
GGGSNGGGNLFPEVAAGGGGGLPFFNLPMNMQPNVQLPVEGWPGNSGGRGPF*

>G1089 (31..2427)

AAGTAAGAGAGCTTCTTAAGGAAGAAGAAGATGGGTTGTGCTCAATCAAAGATCGAGAAC
GAAGAAGCAGTTACTCGTTGCAAAGAACGAAAACAATTGATGAAAGACGCCGTCACTGCT
CGTAACGCTTTCGCCGCCGCTCACTCAGCTTACGCTATGGCTCTTAAAAACACCGGAGCT

GCTCTTTCCGATTACTCTCACGGCGAGTTTTTAGTCTCTAATCACTCGTCTTCCTCCGCA
GCTGCAGCAATCGCTTCTACTTCTTCTCTTCCCACTGCTATATCTCCTCCTCTTCCTTCT
TCCACCGCTCCGGTTTCTAATTCAACCGCTTCTTCTTCCTCCGCTGCGGTTCCTCAGCCG
ATTCCTGATACTCTTCCTCCTCCTCCTCCTCCACCACCGCTTCCTCTTCAACGTGCTGCT
ACTATGCCGGAGATGAACGGTAGATCCGGTGGTGGTCATGCTGGTAGTGGACTCAACGGA
ATTGAAGAAGATGGAGCCCTAGATAACGATGATGATGACGATGATGATGATGATGACTCT
GAAATGGAGAATCGTGATCGTTTGATTAGGAAATCGAGAAGCCGTGGAGGTAGTACTAGA
GGAAATAGGACGACGATTGAAGATCATCATCTTCAGGAGGAGAAAGCTCCGCCACCTCCC
CCTTTGGCGAATTCGCGGCCAATTCCGCCGCCACGTCAGCATCAGCATCAACATCAGCAA
CAGCAACAACAACCTTTCTACGATTACTTCTTCCCTAATGTTGAGAATATGCCTGGAACT
ACTTTAGAAGATACTCCTCCACAACCACAACCACAACCAACAAGGCCTGTGCCTCCTCAA
CCACATTCACCAGTCGTTACTGAGGATGACGAAGATGAGGAGGAGGAAGAGGAGGAAGAG
GAGGAGGAAGAGGAGACGGTGATTGAACGGAAACCACTGGTGGAGGAAAGACCGAAGAGA
GTAGAGGAAGTGACGATTGAATTGGAAAAAGTTACTAATTTGAGAGGGATGAAGAAGAGT
AAAGGGATAGGGATTCCCGGAGAGAGGAGAGGAATGCGAATGCCGGTGACTGCGACGCAT
TTGGCGAATGTATTCATTGAGCTTGATGATAATTTCTTGAAAGCTTCTGAAAGTGCTCAT
GATGTTTCTAAGATGCTTGAAGCTACTAGGCTCCATTACCATTCTAATTTTGCAGATAAC
CGAGGACATATTGATCACTCTGCTAGAGTGATGCGTGTAATTACATGGAATAGATCATTT
AGAGGAATACCAAATGCTGATGATGGGAAAGATGATGTTGATTTGGAAGAGAATGAAACT
CATGCTACTGTTCTTGACAAATTGCTAGCATGGGAAAAGAAGCTCTATGACGAAGTCAAG
GCTGGCGAACTCATGAAAATCGAGTACCAGAAAAAGGTTGCTCATTTAAATCGGGTGAAG
AAACGAGGTGGCCACTCGGATTCATTAGAGAGAGCTAAAGCAGCAGTAAGTCATTTGCAT
ACAAGATATATAGTTGATATGCAATCCATGGACTCCACAGTTTCAGAAATCAATCGTCTT
AGGGATGAACAACTATACCTAAAGCTCGTTCACCTTGTTGAGGCGATGGGGAAGATGTGG
GAAATGATGCAAATACATCATCAAAGACAAGCTGAGATCTCAAAGGTGTTGAGATCTCTA
GATGTTTCACAAGCGGTGAAAGAAACAAATGATCATCATCACGAACGCACCATCCAGCTC
TTGGCAGTGGTTCAAGAATGGCACACGCAGTTTTGCAGGATGATAGATCATCAGAAAGAA
TACATAAAAGCACTTGGCGGATGGCTAAAGCTAAATCTCATCCCTATCGAAAGCACACTC
AAGGAGAAAGTATCTTCGCCTCCTCGAGTTCCCAATCCCGCAATCCAAAAACTCCTCCAC
GCTTGGTATGACCGTTTAGACAAAATCCCCGACGAAATGGCTAAAAGTGCCATAATCAAT
TTCGCAGCGGTTGTAAGCACGATAATGCAGCAGCAAGAAGACGAGATAAGTCTCAGAAAC
AAATGCGAAGAGACAAGAAAAGAATTGGGAAGAAAAATTAGACAGTTTGAGGATTGGTAC
CACAAATACATCCAGAAGAGAGGACCGGAGGGGATGAATCCGGATGAAGCGGATAACGAT
CATAATGATGAGGTCGCTGTGAGGCAATTCAATGTAGAACAAATTAAGAAGAGGTTGGAA
GAAGAAGAAGAAGCTTACCATAGACAAAGCCATCAAGTTAGAGAGAAGTCACTGGCTAGT
CTTCGAACTCGCCTCCCCGAGCTTTTTCAGGCAATGTCCGAGGTTGCGTATTCATGTTCG
GATATGTATAGAGCTATAACGTATGCGAGTAAGCGGCAAAGCCAAAGCGAACGGCATCAG
AAACCTAGCCAGGGACAGAGTTCGTAAGAACTAATGTAAGATCAGAGTAATGTCTTCTTC
TTCTTTGATCTTGAATATTTAAGCACACACATACATACAACGTATAGCTAAATCTTTATC
ATTGCTTTCTTATATTAAGGTTTTGGCTTTTGTAAGAAGGTTTCTTACATATGAGATTCA
TATAGTGTTTGATTCTTAAGGAACTGTTCTGTTGAGTAATAAGAAAGTTGTGTATTGAAA
TAGAGTTGCATTTGTTAATTTTG
>G1089 Amino Acid Sequence (domain in AA coordinates 425-500)
MGCAQSKIENEEAVTRCKERKQLMKDAVTARNAFAAAHSAYAMALKNTGAALSDYSHGEF
LVSNHSSSSAAAAIASTSSLPTAISPPLPSSTAPVSNSTASSSSAAVPQPIPDTLPPPPP
PPPLPLQRAATMPEMNGRSGGGHAGSGLNGIEEDGALDNDDDDDDDDDDDSEMENRDRLIR
KSRSRGGSTRGNRTTIEDHHLQEEKAPPPPPLANSRPIPPPRQHQHQQQQQQQQPFYDYF
FPNVENMPGTTLEDTPPQPQPQPTRPVPPQPHSPVVTEDDEDEEEEEEEEEEEEETVIER
KPLVEERPKRVEEVTIELEKVTNLRGMKKSKGIGIPGERRGMRMPVTATHLANVFIELDD
NFLKASESAHDVSKMLEATRLHYHSNFADNRGHIDHSARVMRVITWNRSFRGIPNADDGK
DDVDLEENETHATVLDKLLAWEKKLYDEVKAGELMKIEYQKKVAHLNRVKKRGGHSDSLE
RAKAAVSHLHTRYIVDMQSMDSTVSEINRLRDEQLYLKLVHLVEAMGKMWEMMQIHHQRQ
AEISKVLRSLDVSQAVKETNDHHHERTIQLLAVVQEWHTQFCRMIDHQKEYIKALGGWLK
LNLIPIESTLKEKVSSPPRVPNPAIQKLLHAWYDRLDKIPDEMAKSAIINFAAVVSTIMQ
QQEDEISLRNKCEETRKELGRKIRQFEDWYHKYIQKRGPEGMNPDEADNDHNDEVAVRQF
NVEQIKKRLEEEEEAYHRQSHQVREKSLASLRTRLPELFQAMSEVAYSCSDMYRAITYAS
KRQSQSERHQKPSQGQSS*

>G1093 (1..531)
ATGGGTTATCCGGTGGGGTACACTGAGCTCCTCCTCCCAAGAATCTTCCTTCACTTACTC
TCTCTCTTAGGCTTAATACGAACACTCATAGACACGGGTTTTCGGATATTGGGTCTACCC
GACTTTCTCGAATCCGACCCGGTTTCATCGTCATCGTCATGGCTGGAACCACCGTATATG
TCCACGGCGGCGCATCATCACCAAGAAAGCTCATTTTTCTTCCCAGTGGCGGCGAGGCTA
GCTGGAGAAATCTTGCCCGTCATCAGATTCTCGGAGCTAACTCGACCCGGATTCGGATCC
GGATCCGATTGCTGCGCGGTGTGCCTCCACGAGTTCGAGAACGATGACGAGATCCGACGG
CTGACGAATTGTCAACACATATTTCACCGGAGCTGTTTAGACCGTTGGATGATGGGTTAT
AATCAGATGACGTGTCCACTTTGTAGAACGCCGTTTATTTCTGATGAGTTACAAGTTGCT
TTTAACCAACGAGTTTGGTCTGAATCTGAACTTCTCGCAGAATCAAATTAG
>G1093 Amino Acid Sequence (domain in AA coordinates: 105-148)
MGYPVGYTELLLPRIFLHLLSLLGLIRTLIDTGFRILGLPDFLESDPVSSSSSWLEPPYM
STAAHHHQESSFFFPVAARLAGEILPVIRFSELTRPGFGSGSDCCAVCLHEFENDDEIRR
LTNCQHIFHRSCLDRWMMGYNQMTCPLCRTPFISDELQVAFNQRVWSESELLAESN*
>G1127 (191..1351)
GACAGACTCTCTCTGTATGTGTGCGAGAAGCGAGAAGCGAGAGAGAGAGAGAGAGAGTTG
TTAGCTCACACGCTTTCTCTATTTTCTCGGAATTCACAAAACAGAAAGTTTCATCCTTTA
CGAGAATTAAGCCGAAAGAAACAATCTTTGAGTTTGATTTCTTCTTCCTTCCTTCTCTCT
CTCTGCTCTAATGGATTCCAGAGACATCCCACCGTCACATAACCAGCTTCAACCACCACC
GGGAATGTTAATGTCTCATTACCGTAACCCTAACGCCGCCGCTTCACCATTAATGGTTCC
CACTTCCACATCTCAACCGATTCAACACCCTCGTCTTCCTTTTGGCAATCAACAACAATC
TCAAACGTTTCATCAGCAGCAACAACAACAAATGGATCAGAAGACTCTTGAATCTCTTGG
ATTTGGTGATGGATCACCTTCTTCTCAACCGATGCGATTCGGGATCGATGATCAGAATCA
GCAACTGCAAGTGAAGAAGAAGCGAGGAAGGCCGAGAAAGTATACTCCTGATGGTAGCAT
TGCTTTAGGTTTAGCTCCTACGTCTCCTCTTCTCTCTGCAGCTTCTAATTCTTACGGTGA
GGGTGGTGTTGGAGATAGTGGTGGAAATGGAAACTCTGTTGATCCACCTGTTAAACGTAA
CAGAGGAAGGCCTCCTGGTTCTAGTAAGAAACAGCTTGATGCTTTAGGAGGAACTTCAGG
AGTTGGGTTTACACCTCATGTCATTGAAGTGAACACAGGAGAGGACATAGCGTCAAAGGT
GATGGCTTTTTCGGATCAAGGGTCAAGAACAATTTGTATTCTCTCTGCAAGTGGTGCAGT
TTCTAGAGTGATGCTTCGTCAAGCTTCTCATTCTAGTGGAATCGTTACTTATGAGGGACG
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CAGAAGTGGTAACTTGAGTGTGGCTTTGGCTGGACCTGATGGCGGCATCGTAGGTGGCAG
TGTAGTTGGTAATCTAGTAGCTGCAACACAAGTCCAGGTGATAGTGGGAAGCTTTGTTGC
AGAAGCAAAGAAACCGAAACAAAGTAGTGTTAACATTGCTCGGGGGCAGAATCCTGAACC
GGCTTCAGCGCCGGCTAACATGTTGAACTTTGGATCAGTCTCTCAAGGACCATCGAGCGA
GTCATCAGAAGAGAATGAGAGCGGTTCTCCTGCAATGCACCGTGACAATAATAATGGGAT
ATATGGAGCTCAACAACAACAACAACAACAACCTCTTCATCCTCATCAGATGCAAATGTA
CCAACATCTTTGGTCTAATCATGGTCAATAAAATGAAGCGGAAATTAATTTGTTTCCGTT
TTGGTTACGGTTATGGTTTGATTTCTT
>G1127 Amino Acid Sequence (domain in AA coordinates:103-110, 155-162)
MDSRDIPPSHNQLQPPPGMLMSHYRNPNAAASPLMVPTSTSQPIQHPRLPFGNQQQSQTF
HQQQQQQMDQKTLESLGFGDGSPSSQPMRFGIDDQNQQLQVKKKRGRPRKYTPDGSIALG
LAPTSPLLSAASNSYGEGGVGDSGGNGNSVDPPVKRNRGRPPGSSKKQLDALGGTSGVGF
TPHVIEVNTGEDIASKVMAFSDQGSRTICILSASGAVSRVMLRQASHSSGIVTYEGRFEI
ITLSGSVLNYEVNGSTNRSGNLSVALAGPDGGIVGGSVVGNLVAATQVQVIVGSFVAEAK
KPKQSSVNIARGQNPEPASAPANMLNFGSVSQGPSSESSEENESGSPAMHRDNNNGIYGA
QQQQQQPLHPHQMQMYQHLWSNHGQ*
>G1131 (57..758)
TCGACTCCTCTCCTGATTGCTTCACCTTCTTCTTTACTACAGGTTTCAGCTCCTCAATGT
CCATGGATTGCTTAAGCTACTTCTTTAACTACGATCCTCCTGTCCAGCTCCAGGATTGCT
TTATTCCCGAGATGGATATGATTATCCCTGAAACCGATAGTTTCTTCTTCCAATCTCAAC
CGCAACTGGAGTTTCATCAGCCATTGTTTCAAGAAGAAGCTCCTTCACAGACCCACTTTG
ACCCTTTCTGCGACCAGTTTCTTTCTCCGCAAGAAATCTTTCTCCCTAACCCTAAAAACG
AAATCTTCAACGAAACACACGACCTCGATTTCTTTCTCCCCACGCCAAAACGCCAGAGAC
TTGTTAACTCCAGCTACAATTGTAACACTCAAAACCATTTCCAGAGCCGTAACCCGAATT
TCTTCGACCCTTTCGGCGACACTGATTTCGTTCCAGAATCTTGTACCTTCCAGGAGTTTC
GAGTTCCGGATTTCTCTTTAGCTTTCAAGGTAGGCCGGGGAGATCAAGATGACTCAAAGA

AACCGACGCTTTCATCTCAGAGCATCGCGGCTAGAGGGAGGAGAAGAAGAATTGCAGAGA
AGACTCACGAGCTCGGAAAACTCATCCCCGGTGGCAATAAACTTAACACCGCCGAGATGT
TCCAAGCCGCCGCTAAGTATGTCAAGTTTTTGCAGAGTCAAGTTGGGATTCTCCAACTGA
TGCAGACCACAAAGAAGGTAATAACCAACCCCAAATAAGAACTTTATCATCCAATTGAAA
CTCTAATCGTGTTTTCTCACAAGCTTCTTAATTTGTTTACGCAGGGTAGCTCTAATGTGC
AAATGGAAACTCAGTATTTGCTTGAATCGCAAGCAATCCAGGAGAAGTTATCAACAGAGG
AAGTGTGTTTGGTACCGTGTGAAATGGTTCAAGATCTAACAACTGAAGAAACCATTTGCA
GAACCCCGAATATTTCTCGAGAAATCAACAAGTTACTGTCTAAACATCTGGCTAACTAGT
TTTAGTTTCAAGCCTGAAGTTCTCTATGCCTAAATTTGTGTCTGTTATCGTTGTTTTGTC
TTCTTAGTTAGTGTTTTGTCTTGTTGATTTAGGGGCTAATTATCCTGGTTAATCTCCTCT
TAACTGGGAA

>G1131 Amino Acid Sequence (domain in AA coordinates: 173-220)
MSMDCLSYFFNYDPPVQLQDCFIPEMDMIIPETDSFFFQSQPQLEFHQPLFQEEAPSQTH
FDPFCDQFLSPQEIFLPNPKNEIFNETHDLDFFLPTPKRQRLVNSSYNCNTQNHFQSRNP
NFFDPFGDTDFVPESCTFQEFRVPDFSLAFKVGRGDQDDSKKPTLSSQSIAARGRRRRIA
EKTHELGKLIPGGNKLNTAEMFQAAAKYVKFLQSQVGILQLMQTTKKVITNPK*

>G1145 (243..1142)
GTGATTTCTCTCTGCCATTTCCTTCGATTTGATTTCTGGGTTCTCTTCTTCTCGTCTCTC
TTCTGCATGTTTCGCCACTCTACCTTAGAAAAAAGGTTACTTTCGCCTCCGATTTAGGCT
CGATTTGATGAATTCGTCGTCGTGTGGCTATTTATCAAATTGAGCATTAGGGTTTCTGAT
TTGTGGGTTCAGAATTGTTTTTATCTATCTGTCTTGTTGTTTTTTGTCCGCTACAAAAGC
CTATGGATTCTCAGAGGGGTATTGTTGAACAAGCTAAATCTCAGTCCTTGAATAGGCAAA
GCTCTCTTTACAGCTTAACACTTGATGAGGTTCAAAATCACTTGGGGAGTTCTGGTAAAG
CTCTGGGAAGCATGAACCTTGATGAGCTTTTGAAGAGTGTCTGTTCTGTTGAAGCTAATC
AGCCATCGTCTATGGCTGTCAATGGTGGAGCAGCTGCTCAGGAGGGTCTTTCTCGCCAGG
GGAGTTTGACTTTGCCTCGGGATCTCAGCAAAAAGACTGTTGATGAGGTTTGGAAAGACA
TTCAGCAGAATAAGAATGGAGGTAGTGCTCATGAGAGGAGGGATAAGCAGCCTACACTTG
GGGAAATGACGCTTGAAGACCTGTTGTTGAAAGCAGGAGTGGTCACTGAGACTATCCCTG
GTTCGAACCATGATGGTCCTGTTGGTGGTGGTAGTGCTGGTTCAGGTGCTGGTTTAGGGC
AAAACATTACTCAAGTTGGCCCATGGATTCAATATCATCAGCTCCCATCAATGCCACAGC
CTCAAGCATTTATGCCCTATCCGGTTTCAGATATGCAAGCAATGGTGTCTCAGTCTTCTT
TGATGGGTGGTTTGTCAGATACACAAACTCCTGGAAGGAAGAGGGTAGCTTCAGGAGAAG
TTGTAGAGAAGACTGTAGAGAGGAGGCAGAAGAGAATGATAAAGAACAGAGAGTCTGCTG
CTCGTTCCCGAGCTAGGAAACAGGCTTACACTCATGAGCTAGAGATCAAAGTTTCACGGT
TAGAAGAAGAAAACGAAAGACTCAGGAAGCAAAAGGAGGTGGAAAAATCCTCCCAAGTGT
ACCACCGCCTGATCCCAAGCGGCAGCTCCGACGGACAAGCTCGGCTCCTTTCTGATCTCT
AAACTCTTTTTGTCTTTTTCTTTTTTTCTCTTCTGTGTCGGTTCACTTATAAAAAAGAGA
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>G1145 Amino Acid Sequence (conserved domain in AA coordinates:227-270)
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QAFMPYPVSDMQAMVSQSSLMGGLSDTQTPGRKRVASGEVVEKTVERRQKRMIKNRESAA
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>G1229 (123..1217)
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CGATGCAGGAGATAATACCGGATTTTCTTGAAGAGTGTGAATTTGTCGACACTTCACTAG
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>G1229 Amino Acid Sequence (domain in AA coordinates: 102-160)
MQEIIPDFLEECEFVDTSLAGDDLFAILESLEGAGEISPTAASTPKDGTTSSKELVKDQD
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QTFC*
>G1246 (1..1746)
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AGGTAG
>G1246 Amino Acid Sequence (domain in AA coordinates: 27-139)

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GHYDSSDNLCSLQDLKSKEEESLQMNTMQEDIAKLLDWGSDSGEISNGQSSVVTDDNLVL
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>G1255 (138..1388)
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>G1255 Amino Acid Sequence (domain in aa coordinates: 18-56)
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DDRKDVDGTVPFELSFDYESSHKTSEEEVMKNVESSGECVVKVKEEEHKNVLMLRLNYDS
VISTWGGQGPPWSSGEPPERDMDISGWPAFSMVENGGESTHQKQYVGGCLPSSGFGDGGR
EARVSRYREKRRTRLFSKKIRYEVRKLNAEKRPRMKGRFVKRASLAAAASPLGVNY*
>G1304 (1..978)
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>G1304 Amino Acid Sequence (conserved domain in AA coordinates:13-118)
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>G1318 (7..849)
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A
>G1318 Amino Acid Sequence (domain in AA coordinates: 20-123)
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>G1320 (39..788)
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>G1320 Amino Acid Sequence (domain in AA coordinates: 5-108)
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EGAIDQTKRPMEFYNFLQVNTDSKIHELIDNSRKDEEEDVDQNNRIRNENCVPFFDFLSV
GNSASQGLC*
>G1330 (36..959)
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>G1330 Amino Acid Sequence (domain in AA coordinates: 28-134)
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VHDNGSF*
>G1352 (79..900)
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>G1352 Amino Acid Sequence (domain in AA coordinates: 108-129,167-188)
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>G1354 (1..1047)
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>G1354 Amino Acid Sequence (domain in AA coordinates: TBD)
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VNKDPSDNSSNETFHHLSEEQAATMVSMNASSSSSPCSFYSWAQNTHT*
>G1360 (1..1257)
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>G1360 Amino Acid Sequence (conserved domain in AA coordinates:18-174)
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SFLLNTSSDSTFLGEFTSHIDLSAVLAQEQCPPLVSLPQEYQETGFEGNGIMKNMRGSNE
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>G1364 (1..537)
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TGTCAAAGAGAGAAAAGGAAGACTATTAATGGAGATGATTTGCTTTGGGCAATGGCTACT
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>G1364 Amino Acid Sequence (conserved domain in AA coordinates:29-120)
MAESQAKSPGGCGSHESGGDQSPRSLHVREQDRFLPIANISRIMKRGLPANGKIAKDAKE
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>G1379 (68..622)
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>G1379 Amino Acid Sequence (domain in AA coordinates: 18-85)
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ESKH*
>G1384 (33..977)
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>G1384 Amino Acid Sequence (domain in AA coordinates: TBD)
MADLFGGGHGGELMEALQPFYKSASTSASNPAFASSNDAFASAPNDLFSSSSYYNPHASL
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SQPGFMTQPGPSSGSVSKPAKLYRGVRQRHWGKWVAEIRLPRNRTRLWLGTFDTAEEAAL
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>G1399 (261..1475)
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>G1399 Amino Acid Sequence (domain in AA coordinates: 86-93)
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>G1415 (60..680)
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>G1415 Amino Acid Sequence (domain in AA coordinates: TBD)
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GDNDISRFDTCISGGYSNWDSFHSPL*
>G1417 (32..1501)
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>G1417 Amino Acid Sequence (domain in AA coordinates: 239-296)
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>G1442 (1..1293)
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>G1442 Amino Acid Sequence (domain in AA coordinates: 172-223)
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>G1454 (86..1180)
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>G1454 Amino Acid Sequence (conserved domain in AA coordinates:9-178)
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WYSS*
>G1459 (1..1272)
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>G1459 Amino Acid Sequence (conserved domain in AA coordinates:10-152)
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KKL*
>G1460 (87..995)
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>G1460 Amino Acid Sequence (domain in AA coordinates: TBD)
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EPEPELQVEQPGKENLLGMSVDDLIEPMNQQEEPQGPHLAPNDDEFIRGLRHVDREPVEY
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PG*
>G147 (37..672)
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CTCAAGAAGGCTAAGGAGCTCTCTGTGCTCTGTGATGCCGAGATCGGTGTTGTGATCTTC
TCTCCTCAGGGCAAGCTCTTTGAGCTCGCTACTAAAGGAACAATGGAGGGAATGATTGAT
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TGAATTTATGGATT
>G147 Amino Acid Sequence (domain in AA coordinates: 2-57)
MARGKIQLKRIENPVHRQVTFCKRRTGLLKKAKELSVLCDAEIGVVIFSPQGKLFELATK
GTMEGMIDKYMKCTGGGRGSSSATFTAQEQLQPPNLDPKDEINVLKQEIEMLQKGISYMF
GGGDGAMNLEELLLLLEKHLEYWISQIRSAKMDVMLQEIQSLRNKEGVLKNTNKYLLDKIE
ENNNSILDANFAVMETNYSYPLTMPSEIFQF*
>G1471 (1..735)
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GCCCTTGGCGGTCACGGAACCACCCACAAGGAGGACCGAGAATTGGAGAGGCAACAGATC
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AGCAGCAGCAGCAACAACGTTAACCCATTGCTTAATGTTGGAGTCCCTAGAGGAACCACA
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TCTAGTCACTCATAA
>G1471 Amino Acid Sequence (domain in AA coordinates: 49-70)
MENQSMSSSSSSTHKHDQKLKSSVVAMEVLEEKETVNNPPQYYNKIYICYLCKRAFPTPH
ALGGHGTTHKEDRELERQQIESRLSNKDKSNLLFGGSSQDVLSNDNHLGLSLGPLKSIEG
SSSSNNVNPLLNVGVPRGTTDMNMNNYSSHALSTDDINLDLTLGPSKSIGDSNNIINNNT
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SSHS*
>G1475 (1..645)
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GCTCAAGCACTTGGAGGCCACATGAATGTTCATAGAAGAGACAGAGCAAAACTCAGGCAG
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>G1475 Amino Acid Sequence (domain in AA coordinates: 51-73)
MKRTHLASFSNRDKTQEEEGEDGNGDNRVIMNHYKNYEAGLIPWPPKNYTCSFCRREFRS
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LMNKKDDQVMGLELGMSLRNPNQVLDLELRLGYL*
>G1477 (1..606)
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GCATTTTTGGCGCATTTGAACCGACCAGAACCAGATCTTTACGCGTACTCGTATTCGTAT
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CTGTGA
>G1477 Amino Acid Sequence (domain in AA coordinates: 29-48)
MLSSDSNYASDISDDASATGSIENPIYKCKYCPRKFDKTQALGGHQNAHRKEREVEKQQK
AFLAHLNRPEPDLYAYSYSYHHSFPNQYALPPGFEQPQYKVDRSYKMSMVYNQYVGSSSS
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TEEMDAEKENDGSSLSLSLKL*
>G1487 (1..1020)
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TTCTCTGTAGACGACTTGCTTGACTTGTCAAACGATGACGTTTTGCCGACGAAGAAACT
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GACGCTCTTCGCCGGAGCAGCGATTTCTCCGGCTGTGACGACTTTGGTTCTCTCCCTACA
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>G1487 Amino Acid Sequence (domain in AA coordinates:251-276).
MEQAALKSSVRKEMALKTTSPVYEEFLAVTTAQNGFSVDDFSVDDLLDLSNDDVFADEET
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LHSNHHRKVIEMRRKKEPTSDNETGLNQLVQSPQAVPSF*
>G1492 (149..919)
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>G1492 Amino Acid Sequence (domain in AA coordinates: 34-83)
MGKSSGRNGNGSFNGNKFHGVRPYVRSPVPRLRWTPDLHRCFVHAVEILGGQHRATPKLV
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>G1531 (1..666)
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GTGACCGTTAATGGAACCATATGGAATCTAATTGATCCGAGTCAGGGAAGGAATGGATTA
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CTGTGA
>G1531 Amino Acid Sequence (domain in AA coordinates: 41-77)
MCESSNKVRVSPYPLRSSRTDKHKASESPIETGWEDVRGCHPYMCDTSVRHSNCFKQFRR
KTIKKRLYPKTLHCPLCRGEVSETTKVTSTARRFMNAKPRSCSVEDCKFSGTFSQLTKHL
KTEHRGIVPPKVDPLRQQRWEMMERHSEYVELMTAAGISRMAEVMQQQLPQDQNHPHVFQ
VTVNGTIWNLIDPSQGRNGLGITNYSAMQFVPLSINHSRTL*
>G1540 (122..997)
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>G1540 Amino Acid Sequence (domain in AA coordinates: 35-98)
MEPPQHQHHHHQADQESGNNNNKSGSGGYTCRQTSTRWTPTTEQIKILKELYYNNAIRSP
TADQIQKITARLRQFGKIEGKNVFYWFQNHKARERQKKRFNGTNMTTPSSSPNSVMMAAN
DHYHPLLHHHHGVPMQRPANSVNVKLNQDHHLYHHNKPYPSFNNGNLNHASSGTECGVVN
ASNGYMSSHVYGSMEQDCSMNYNNVGGGWANMDHHYSSAPYNFFDRAKPLFGLEGHQDEE
ECGGDAYLEHRRTLPLFPMHGEDHINGGSGAIWKYGQSEVRPCASLELRLN*
>G1544 (1..2178)
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TCTACAATATTTTCTGGTGTTGAAGGAGAAGATATCAGAGTGATGACAATGAAGAGCGTG
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CCTTGTCAGACTGCTTGA

>G1544 Amino Acid Sequence (domain in AA coordinates: 64-124)
MSQSNMVPVANNGDNNNDNENNNNNNNNNGGTDNTNAGNDSGDQDFDSGNTSSGNHGEGLG
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TQNKNQQERFENSELRNLNNHLRSENQRLREAIHQALCPKCGGQTAIGEMTFEEHHLRIL
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PCQTA*

>G156 (39..755)
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>G156 Amino Acid Sequence (domain in AA coordinates: 2-57)
MGRGKIEIKKIENQTARQVTFSKRRTGLIKKTRELSILCDAHIGLIVFSATGKLSEFCSE
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NELDGLERQLEHSVLKVRERKRRMLEEDNNNMYRWLHEHRAAMEFQQAGIDTKPGEYQQF
IEQLQCYKPGEYQQFLEQQQQQPNSVLQLATLPSEIDPTYNLQLAQPNLQNDPTAQND*
>G1584 (160..1281)
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>G1584 Amino Acid Sequence (domain in AA coordinates: TBD)
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>G1587 (1..816)
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TCATCAGGAGAACACGATATTGATGAACGGAAAAACAACATTCCTGCGGCGGCGACTTTG
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CGCCGCCGTCGTGAAGGTGGTGCTATTATCAAACCACATAAAGACGTCAAGGATTCATCA
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ACATGGAGAAATCTTGTTACTTGGTCGATAACTCAACAACCGGAAGAGATTAATATCGAC
GAAAATGTCAACGGAGAAGAAGAAGAAACGAGGGACAACCGGACTTTAAATCTCTTTCCG
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>G1587 Amino Acid Sequence (conserved domain in AA coordinates:61-121)
MGYISNNNLINYLPLSTTQPPLLLTHCDINGNDHHQLITASSGEHDIDERKNNIPAAATL
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>G1588 (1..2232)
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>G1588 Amino Acid Sequence (domain in AA coordinates: 66-124)
MYHPNMFESHHMFDMTPKSTSDNDLGITGSREDDFETKSGTEVTTENPSGEELQDPSQRP
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NSLIKCTVERIKAAVSCDVGGGA*
>G1589 (179..2221)
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>G1589 Amino Acid Sequence (conserved domain in AA coordinates:384-448)
MAAYFHGNPPEISAGSDGGLQTLILMNPTTYVQYTQQDNDSNNNNNSNNSNNNNTNTNTN
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GMNIQNQKRYVAQLLPDFVA*

>G160 (38..784)
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>G160 Amino Acid Sequence (domain in AA coordinates: 7-62)
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SSYNFNQS*
>G1636 (19..666)
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>G1636 Amino Acid Sequence (domain in AA coordinates: 100-165)
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>G1642 (1..1077)
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>G1642 Amino Acid Sequence (domain in AA coordinates: TBD)
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>G1747 (1..777)
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>G1747 Amino Acid Sequence (domain in AA coordinates: 11-114)
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>G1749 (59..535)
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>G1749 Amino Acid Sequence (conserved domain in AA coordinates:84-155)
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>G1751 (117..923)
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>G1751 Amino Acid Sequence (domain in AA coordinates: TBD)
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EWMNMMMMMDFGNGDSSDSGNTIADMFQ*
>G1752 (25..756)
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AAGCAGAGTGTTGTGAAGCAAGAAAGTGGTACACTTGTGGTTTTTGAAGATTTAGGTGCT
GAGTATTTAGAACAACTTCTTATGAGCTCATGTTGATCTTGTAATTGATTTCAGCAAAAG
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ATTTCTTTGGTTCTCTTATTTTTTGTTTGTTGTATCCAAATGAAATTATTGGAAGAGATG
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>G1752 Amino Acid Sequence (domain in AA coordinates: TBD)
MEYSQSSMYSSPSSWSSSQESLLWNESCFLDQSSEPQAFFCPNYDYSDDFFSFESPEMMI
KEEIQNGDVSNSEEEEKVGIDEERSYRGVRKRPWGKFAAEIRDSTRNGIRVWLGTFDKAE
EAALAYDQAAFATKGSLATLNFPVEVVRESLKKMENVNLHDGGSPVMALKRKHSLRNRPR
GKKRSSSSSSSSSNSSSCSSSSSTSSTSRSSSKQSVVKQESGTLVVFEDLGAEYLEQLLM
SSC*
>G1763 (33..977)
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ATCCTGCGTTTGCGTCCTCAAACGATGCGTTTGCGTCTGCCCCAAACGACCCATTTTTCTT
CTTCTTCTTACTATAATCCTCATGCATCTTTCTTCCCTTCACATTCCACAACCACTTACC
CGGATATTTATTCTGGATCCATGACCTATCCATCTTCATTCGGGTCGGATCTTCAACAAC
CCGAAAACTACCAATCTCAGTTCCATTACCAAAACACTATCACTTACACTCACCAAGACA
ACAACACTTGCATGCTCAACTTCATTGAGCCGAGCCAACCGGATTTTATGACCCAACCGG
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TAGCTGAGCCGAAGAATCAGCCGGGCAAAACGGAGAGGACGTCGAGGAAACGAGCTAAAG
CCGCGGCTTCTTCAGCTGAGCAGCCGTCAGCGCCACAACAACATTCCGGGTCGGGTGAAA
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AGATGCCATGGAATGAAAATTTCATGCTCGGCAAGTGTCCTTCTTATGAGATAGATTGGG
CTTCAATTTTATCGTGAAAAATTAGGATTCAATTCATTTTTATTCATTTTAACTTGTTTG
TATTTTCTTTTAAACTTTAGGGTTATTAGCTGTGCGTAAAATTTGTAATTTAGCATTTTG
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>G1763 Amino Acid Sequence (conserved domain in AA coordinates:140-209)
MADLFGGGHGGELMEALQPFYKSASTSASNPAFASSNDAFASAPNDPFSSSSYYNPHASF
FPSHSTTTYPDIYSGSMTYPSSFGSDLQQPENYQSQFHYQNTITYTHQDNNTCMLNFIEP
SQPDFMTQPGPSSGSVSKPAKLYRGVRQRHWGKWVAEIRLPRNRTRLWLGTFDTAEEAAL
AYDRAAFKLRGDSARLNFPALRYQTGSSPSDVGEYGPIQAAVDAKLEAILAEPKNQPGKT
ERTSRKRAKAAASSAEQPSAPQQHSGSGESDGSGSPTSDVMVQEMCQEPEMPWNENFMLG
KCPSYEIDWASILS*
>G1766 (32..1216)
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GAAAATACATGCACACTAGTGTTATTTATACTTAAAGATGGAAGGGGAAAAACAAGGAGT
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>G1766 Amino Acid Sequence (domain in AA coordinates: 10-153)
MNSFSQVPPGFRFHPTDEELVDYYLRKKVASKRIEIDIIKDVDLYKIEPCDLQELCKIGN
EEQSEWYFFSHKDKKYPTGTRTNRATKAGFWKATGRDKAIYIRHSLIGMRKTLVFYKGRA
PNGQKSDWIMHEYRLETSENGTPQEEGWVVCRVFKKKLAATVRKMGDYHSSPSQHWYDDQ
LSFMASEIISSSPRQFLPNHHYNRHHHQQTLPCGLNAFNNNNPNLQCKQELELHYNQMVQ
HQQQNHHLRESMFLQLPQLESPTSNCNSDNNNNTRNISNLQKSSNISHEEQLQQGNQSFS
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INLPENDSERVVEMGEEYSNAHAASTSSSCQIDL*
>G1767 (1..1596)
ATGGATACTCTCTTTAGACTAGTCAGTCTCCAACAACAACAACAATCCGATAGTATCATT
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ACTTACTACTCTCCTTTCACTACTCCCACCCAATACCATCCCGCCACATCATCAACCCCT
TCCTCCACCGCCGCAGCCGCAGCTTTAGCCTCGCCTTACTCCTCCTCCGGCCACCATAAT
GACCCTTCCGCGTTCTCCATACCTCAAACTCCTCCGTCCTTCGACTTCTCAGCCAATGCC
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CAAACGGCGTCGCATCGGATGATGAAAGAGATCGGAAACCGAATGGAGAAATTCGCTAGG
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TGCTTCGAGTCATGGGAAGAGAGTTTTCCAAGGACGAGCAACGAGAGGTTGATGCTAGAG
CGTGCAGCGGGACGTGCGATCGTTGATCTTGTGGCTTGTGAGCCGTCGGATTCCACGGAG
AGGCGAGAGACAGCGAGGAAGTGGTCGAGGAGGATGAGGAATAGTGGGTTTGGAGCGGTG
GGGTATAGTGATGAGGTGGCGGATGATGTCAGAGCTTTGTTGAGGAGATATAAAGAAGGT
GTTTGGTCGATGGTACAGTGTCCTGATGCCGCCGGAATATTCCTTTGTTGGAGAGATCAG
CCGGTGGTTTGGGCTAGTGCGTGGCGGCCAACGTAA
>G1767 Amino Acid Sequence (domain in AA coordinates: 255-272)
MDTLFRLVSLQQQQQSDSIITNQSSLSRTSTTTTGSPQTAYHYNFPQNDVVEECFNFFMD
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AANGAILEAVDGEAKIHIVDISSTFCTQWPTLLEALATRSDDTPHLRLTTVVVANKFVND
QTASHRMMKEIGNRMEKFARLMGVPFKFNIIHHVGDLSEFDLNELDVKPDEVLAINCVGA
MHGIASRGSPRDAVISSFRRLRPRIVTVVEEEADLVGEEEGGFDDEFLRGFGECLRWFRV
CFESWEESFPRTSNERLMLERAAGRAIVDLVACEPSDSTERRETARKWSRRMRNSGFGAV
GYSDEVADDVRALLRRYKEGVWSMVQCPDAAGIFLCWRDQPVVWASAWRPT*
>G1778 (1..627)
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AATTCTAACAACATCTCCGGCGACTTTTATATTCACGGAGGAAACGCTAAGACTTCTTCG
TACAAGAAGGGTGGTGTTGCTCATAGCCTACCTCGCCGTTGTGCTAGCTGCGACACCACT
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GGTTCATCAGCGGCAGAAGTCCCAGTAGAGAATTCGTACAACGGAGGTGGAAACTATTAC
AGTCATCATCATCATCACTATGCCTCGTCGTCGCCGTCGTGGGCTCATCAGAACACACAA
AGAGTTCCATATTTCTCACCGGTTCCGGAGATGGAATATCCCTACGTGGATAACGTCACG
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>G1778 Amino Acid Sequence (domain in AA coordinates:94-119)
MMGYQTNSNFSMFFSSENDDQNHHNYDPYNNFSSSTSVDCTLSLGTPSTRLDDHHRFSSA
NSNNISGDFYIHGGNAKTSSYKKGGVAHSLPRRCASCDTTSTPLWRNGPKGPKSLCNACG
IRFKKEERRATARNLTISGGGSSAAEVPVENSYNGGGNYYSHHHHHYASSSPSWAHQNTQ
RVPYFSPVPEMEYPYVDNVTASSFMSWN*
>G1789 (108..413)
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CAATGTCTTCTTATGGCTCTGGCTCATGGACTGTTAAGCAGAACAAAGCCTTTGAGCGTG
CTCTAGCAGTCTATGACCAAGACACTCCGGACCGTTGGCACAATGTTGCTAGAGCTGTTG
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AGCAACAAAACCTAACTACGTATGATCGTCAAAATAAAAGAGAATCACTTCAGAGAGATG
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TAAGAAATGGTTTTTTTTTCGAGGCAACAAAAAAAAAA
>G1789 Amino Acid Sequence (domain in AA coordinates: 1-50)
MASGSMSSYGSGSWTVKQNKAFERALAVYDQDTPDRWHNVARAVGGKTPEEAKRQYDLLV
RDIESIENGHVPFPDYKTTTGNSNRGRLRDEEKRMRSMKLQ*
>G1790 (63..1346)

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AGCTGCTTGAGGAAGGATGTAGCATTGACTCTTTGCTTGATGACATTCCTCAGCCTGACA
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>G1790 Amino Acid Sequence (conserved domain in AA coordinates:217-316)
MENFVDENGFASLNQNIFTRDQEHMKEEDFPFEVVDQSKPTSFLQDFHHLDHDHQFDHHH
HHGSSSSHPLLSVQTTSSCINNAPFEHCSYQENMVDFYETKPNLMNHHHFQAVENSYFTR
NHHHHQEINLVDEHDDPMDLEQNNMMMMRMIPFDYPPTETFKPMNFVMPDEISCVSADND
CYRATSFNKTKPFLTRKLSSSSSSSSWKETKKSTLVKGQWTAEEDRVLIQLVEKYGLRKW
SHIAQVLPGRIGKQCRERWHNHLRPDIKKETWSEEEDRVLIEFHKEIGNKWAEIAKRLPG
RTENSIKNHWNATKRRQFSKRKCRSKYPRPSLLQDYIKSLNMGALMASSVPARGRRRESN
NKKKDVVVAVEEKKKEEEVYGQDRIVPECVFTDDFGFNEKLLEEGCSIDSLLDDIPQPDI
DAFVHGL*
>G1791 (36..455)
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ACGCGGCTCGGGCTTATGATAGAGCAGCTTTCGGCATGAGAGGCCAAAGGGCCATTCTCA
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TGGCTTCCTCGTCGTCGGGATATAGAGGAGGAGGTGGTGGTGATGATGGGAGGGAAGTTA
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AAAAAAAAA
>G1791 Amino Acid Sequence (domain in AA coordinates: TBD)
MERIESYNTNEMKYRGVRKRPWGKYAAEIRDSARHGARVWLGTFNTAEDAARAYDRAAFG
MRGQRAILNFPHEYQMMKDGPNGSHENAVASSSSGYRGGGGGDDGREVIEFEYLDDSLLE
ELLDYGERSNQDNCNDANR*
>G1793 (59..1783)
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AACTACTACTAATTTCCCCATTACAAACTACGAGAAAGAAGTAGAGGAAATGAAGCACAT
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TTCGATGTATCGAGGAGTTACAAGGCATCACCAACATGGAAGATGGCAAGCAAGGATCGG
CCGAGTCGCCGGAAACAAAGACCTCTACTTGGGAACTTTTAGCACTGAGGAAGAAGCAGC
AGAAGCTTACGATATAGCTGCAATAAAGTTTAGAGGACTTAATGCAGTGACCAACTTCGA
GATCAACCGGTACGACGTGAAAGCCATTCTAGAGAGTAGCACTCTTCCCATCGGAGGAGG
CGCAGCTAAACGGCTCAAAGAAGCTCAAGCTCTTGAGTCTTCAAGGAAACGCGAGGCGGA
GATGATAGCCCTTGGTTCAAGTTTCCAGTACGGTGGTGGCTCGAGCACAGGCTCTGGCTC
CACCTCATCAAGACTTCAGCTTCAACCTTACCCTCTAAGCATTCAACAACCATTAGAGCC
TTTTCTATCTCTTCAGAACAATGACATCTCTCATTACAACAACAACAATGCTCACGATTC
CTCCTCTTTTAATCACCATAGCTATATCCAGACACAACTTCATCTCCACCAACAGACCAA
CAATTACTTGCAGCAACAGTCGAGCCAGAACTCTCAGCAGCTCTACAATGCGTATCTTCA
TAGCAATCCGGCTCTGCTTCATGGACTTGTCTCTACCTCTATCGTTGACAACAATAATAA
CAATGGAGGCTCTAGTGGGAGCTACAACACTGCAGCATTTCTTGGGAACCACGGTATTGG
TATTGGGTCCAGCTCGACTGTTGGATCGACCGAGGAGTTTCCAACCGTTAAAACAGATTA
CGATATGCCTTCCAGTGATGGAACCGGAGGGTATAGTGGTTGGACCAGTGAGTCTGTTCA
GGGGTCAAACCCTGGTGGTGTTTTCACTATGTGGAATGAGTAAACAAGGATCTCTTTCTT
GCGGCACAAGGAATGGGT

>G1793 Amino Acid Sequence (conserved domain in AA coordinates:179-255, 281-349)

MNSNNWLGFPLSPNNSSLPPHEYNLGLVSDHMDNPFQTQEWNMINPHGGGGDEGGEVPKV
ADFLGVSKPDENQSNHLVAYNDSDYYFHTNSLMPSVQSNDVVVAACDSNTPNNSSYHELQ
ESAHNLQSLTLSMGTTAGNNVVDKASPSETTGDNASGGALAVVETATPRRALDTFGQRTS
IYRGVTRHRWTGRYEAHLWDNSCRREGQSRKGRQVYLGGYDKEDKAARSYDLAALKYWGP
STTTNFPITNYEKEVEEMKHMTRQEFVAAIRRKSSGFSRGASMYRGVTRHHQHGRWQARI
GRVAGNKDLYLGTFSTEEEAAEAYDIAAIKFRGLNAVTNFEINRYDVKAILESSTLPIGG
GAAKRLKEAQALESSRKREAEMIALGSSFQYGGGSSTGSGSTSSRLQLQPYPLSIQQPLE
PFLSLQNNDISHYNNNNAHDSSSFNHHSYIQTQLHLHQQTNNYLQQQSSQNSQQLYNAYL
HSNPALLHGLVSTSIVDNNNNNNGGSSGSYNTAAFLGNHGIGIGSSSTVGSTEEFPTVKTD
YDMPSSDGTGGYSGWTSESVQGSNPGGVFTMWNE*

>G1795 (27..422)

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CTAGAGCCTATGACCAAGCTGCTTACTCCATGAGAGGCCAAGCAGCAATCCTTAACTTCC
CTCATGAGTATAACATGGGGAGTGGTGTCTCTTCTTCCACCGCCATGGCTGGATCTTCCT
CCGCCTCCGCCTCCGCTTCTTCTTCTAGGCAAGTTTTTGAATTTGAGTACTTGGATG
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>G1795 Amino Acid Sequence (domain in AA coordinates: 12-80)

MDQGGRGVGAEHGKYRGVRRRPWGKYAAEIRDSRKHGERVWLGTFDTAEEAARAYDQAAY
SMRGQAAILNFPHEYNMGSGVSSSTAMAGSSSASASASSSSRQVFEFEYLDDSVLEELLE
EGEKPNKGKKK*

>G1800 (61..894)

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CCACAAAACGCTCTTTGTCAGTACCGTGGAGTCAGGCAAAGGACTTGGGGCAAATGGGTG
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GAAGAAGCAGCTATGGCTTATGATGAGGCTGCCTTGAAACTCTATGGGCACGACGCATAC
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GAAGAAACTGGAAGTCCTTTCAGAACTGAGAATTTCAGCTGGGATACCCTGATCGAGATG
CCAAGAAGTGAAACCACAACTATGCAATTTGACTCCAGCAACTTCGGAAGCTATGATTTT
GAGGATGATGTATCCTTCCCTTCCATCTGGGACTACTACGGAAGCTTAGATTGAGTAAAA
GCAATTTAAGGTAGATCAAGATTCAGAAGTACACAAATGGTTTTGGATTTAGTGTAGCGT
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TCAGTGTACAACCGAGTTGTTCGCTTTTTTTGGTATATTAATGAAGCATGTTCATTTTTT
CGCTAAAAAAAAAAAAAAAAAAAAAAAA
>G1800 Amino Acid Sequence (domain in AA coordinates: TBD)
MEKSSSMKQWKKGPARGKGGPQNALCQYRGVRQRTWGKWVAEIREPKKRARLWLGSFATA
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NAQPSVHIIQQRLEELKKTGLLSQSYSSSSSSTESKTNTSFLDEKTSKGETDNMFEGGDQ
KKPEIDLTEFLQQLGILKDENEAEPSEVAECHSPPPWNEQEETGSPFRTENFSWDTLIEM
PRSETTTMQFDSSNFGSYDFEDDVSFPSIWDYYGSLD*
>G1806 (1..1356)
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GAAGAAGCTATCGATTTAAGTCCAAATGTCACTATTGCTTCAGCTAACTTACACTACACG
ACGTTTGATACGGTTATGGATTGTGGTGGTGGTGGTGGTGGCTTGAGGGAGAGACTTGAA
GGAGGAGAAGAGGAGTGTTTGGACACAGGGCAATTAGTGTACCAGAAAGGGACAAGATTA
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CTAGAGGAAGAGCTCAAAAGAGCTCGCCAACAGGGATCTTTGGTTGAAAGAGGAGTTTCA
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>G1835 (1..969)
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>G187 Amino Acid Sequence (domain in AA coordinates: 172-228)
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GEDSGKSRRKRELVGEEDQISKKVGKTKKTEVKKQREPRVSFMTKSEVDHLEDGYRWRKY
GQKAVKNSPYPRSYYRCTTQKCNVKKRVERSFQDPTVVITTYEGQHNHPIPTNLRGSSAA
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EYELLREIFPSIFFKQEP*
>G1881 (1..519)
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AATGCACCCGCATTCTTTTACTGTGAGATAGATGGTAGTTCCCTTTGTCTACAATGTGAT
ATGGTGGTACATGTTGGTGGGAAGAGAACACATAGGCGGTTTCTATTACTGAGACAGAGA
ATTGAGTTTCCAGGCGATAAGCCTAATCATGCTGACCAACTGGGACTACGGTGTCAAAAG
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>G1881 Amino Acid Sequence (domain in AA coordinates:5-28, 56-79)
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>G1882 (1..1200)
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CACCATCCCCTCCCACCGCAACAGCAACAAACGCCTCCGCAGCTTCACCACAACAACGGT
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AATCCAGGTTACGGATTGGTTACCGGGTCGGGTCAGTATCGACCTAAGAACATTTTCCAT
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>G1882 Amino Acid Sequence (domain in AA coordinates:97-125)
MVFSSFPTYPDHSSNWQQQHQPITTTVGFTGNNINQQFLPHHPLPPQQQTPPQLHHNNG
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FCKACRRYWTRGGALRSVPVGGGCRRNKRTKNSSGGGGGSTSSGNSKSQDSATSNDQYHH
RAMANNQMGPPSSSSSLSSLLSSYNAGLIPGHDHNSNNNNILGLGSSLPPLKLMPPLDFT
DNFTLQYGAVSAPSYHIGGGSSGGAAALLNGFDQWRFPATNQLPLGGLDPFDQQHQMEQQ
NPGYGLVTGSGQYRPKNIFHNLISSSSSASSAMVTATASQLASVKMEDSNNQLNLSRQLF
GDEQQLWNIHGAAAASTAAATSSWSEVSNNFSSSSTSNI*
>G1883 (1..1110)
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>G1883 Amino Acid Sequence (domain in aa coordinates: 82-124)
MDATKWTQGFQEMMNVKPMEQIMIPNNNTHQPNTTSNARPNTILTSNGVSTAGATVSGVS

NNNNNTAVVAERKARPQEKLNCPRCNSTNTKFCYYNNYSLTQPRYFCKGCRRYWTEGGSL
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PVMQDQHHHHVHMSQFLQMPKMEGNGNITHQQQPSSSSSVYGSSSSPVSALELLRTGVNV
SSRSGINSSFMPSGSMMDSNTVLYTSSGFPTMVDYKPSNLSFSTDHQGLGHNSNNRSEAL
HSDHHQQGRVLFPFGDQMKELSSSITQEVDHDDNQQQKSHGNNNNNNNSSPNNGYWSGMF
STTGGGSSW*
>G1884 (1..741)
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CTCAAGTGTCCGAGATGTGATTCAGTCAACACCAAATTCTGCTACTACAACAACTACAGC
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>G1884 Amino Acid Sequence (domain in AA coordinates:43-71)
MMTSSHQSNTTGFKPRRIKTTAKPPRQINNKEPSPATQPVLKCPRCDSVNTKFCYYNNYS
LSQPRHYCKNCRRYWTRGGALRNVPIGGSTRNKNKPCSLQVISSPPLFSNGTSSASRELV
RNHPSTAMMMMSSGGFSGYMFPLDPNFNLASSSIESLSSFNQDLHQKLQQQRLVTSMFLQ
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NNNALL*
>G1891 (1..750)
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>G1891 Amino Acid Sequence (domain in aa coordinates: 27-69)
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SSVGAVGNLFGSLYDIHGGMVTNLHPTRTVRPNHRLAFHDGSFEQDYYDVGSDNLLVNQQ
VGGYGYHMNPVDQFKWNQSFNNTMNMNYNNDSTSGSSRGSDMNVNHDNKKIRYRNSVIMH
PCHLEKDGP*
>G1896 (1..951)
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>G1896 Amino Acid Sequence (domain in aa coordinates: 43-85)
MSSHTNLPSPKPVPKPDHRISGTSQTKKPPSSSVAQDQQNLKCPRCNSPNTKFCYYNNYS
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EDSSKFFPPPTTMDFQLAGLSLNKMNDLQLLNNQEVLDLRPMMSSGRENTPVDVGSGLSL
MGFGDFNNNHSPTGFTTAGASDGNLASSIETLSCLNQDLHWRLQQQRMAMLFGNSKEETV
VVERPQPILYRNLEIVNSSSPSSPTKKGDNQTEWYFGNNSDNEGVISNNANTGGGGSEWN
NGIQAWTDLNHYNALP*
>G1898 (1..630)
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>G1898 Amino Acid Sequence (domain in AA coordinates: 31-59)
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QIGEIEGKSGGDSLIWPGLEISMQTNDVK*
>G1902 (1..615)
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CAAAACAAGAAGACGAAAAACCCGGATCCGGATCCTGATCCACGTAATTCTCAAAAACCG
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>G1902 Amino Acid Sequence (domain in AA coordinates:31-59)
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RRTEPGNNNNNPWTDLAMNRAEKN*
>G1904 (1..924)
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CAGAGTGGTCTCTACCTTCCTTGA
>G1904 Amino Acid Sequence (domain in aa coordinates: 53-95)
MQDIHDFSMNGVGGGGGGGGRFFGGGIGGGGGGDRRMRAHQNNILNHHQSLKCPRCNSLN
TKFCYYNNYNLSQPRHFCKNCRRYWTKGGVLRNVPVGGGCRKAKRSKTKQVPSSSSADKP
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QSGLYLP*
>G1906 (1..795)
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CCTGTTGGAGGAGGCTTTAGGAGGAACAAGAGAAGCAAATCCAGATCGAAATCTACGGTC
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AACCCTAGCAAGTTTCATAGCTACGGTCAAATCCCGGAGTTTAATTCCAACTTGCCCATC
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>G1906 Amino Acid Sequence (domain in AA coordinates:19-47)
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YTSWGGNSSWTGFTSNNSTGHLSF*
>G1913 (1..744)
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GTTCATTTCGCTGACGAATCCAATGATTCCACCAATCTCTTGTTTGGAAGTTGGAGCCCT
TTTGATTTCACTGCCGATGGATGA
>G1913 Amino Acid Sequence (domain in AA coordinates: 27-55)
MERAEALTSSFIWRPNANANAEITPSCPRCGSSNTKFCYYNNYSLTQPRYFCKGCRRYWT
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FDFTADG*
>G1914 (1..945)
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CCTAATGAAGAAGATGAAACTTCTTTGGTGTTTGATGAATGGTGA
>G1914 Amino Acid Sequence (domain in AA coordinates:195-216, 245-266)
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PNEEDETSLVFDEW*
>G1925 (1..945)
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>G1929 (1..366)
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>G1930 (76..1077)
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>G1930 Amino Acid Sequence (domain in AA coordinates: 59-124)
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>G1954 (196..1440)
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>G196 (111..1421)
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>G1965 (1..609)
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>G1976 Amino Acid Sequence (domain in AA coordinates: 219-323)
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>G2107 (79..624)
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>G2151 Amino Acid Sequence (domain in AA coordinates:93-113, 124-144)
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>G2157 (306..1238)
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>G2181 (1..1005)
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>G2340 (274..1275)
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>G2340 Amino Acid Sequence (domain in AA coordinates:14-120)
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>G2346 (1..1011)
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>G2346 Amino Acid Sequence (domain in AA coordinates: 59-135)
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>G237 Amino Acid Sequence (domain in AA coordinates: 11-113)
MAKTKYGERHRKGLWSPEEDEKLRSFILSYGHSCWTTVPIKAGLQRNGKSCRLRWINYLR
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>G2373 (48..1199)
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>G2373 Amino Acid Sequence (domain in AA coordinates:290-350)
MEDDDEIQSIPSPGDSSLSPQAPPSPPILPTNDVTVAVVKKPQPGLSSQSPSMNALALVV
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RGERRIVDDDDDRNGKNNGNVSS*
>G2376 (39..1370)
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>G24 (194..724)
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>G2424 (1..999)
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>G2505 (1..1026)
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>G2512 (64..798)
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>G2513 (69..698)
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>G2513 Amino Acid Sequence (domain in AA coordinates: TBD)
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>G2519 (83..691)
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>G2520 (133..1197)
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>G2520 Amino Acid Sequence (domain in AA coordinates: 135-206)
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HALSQAVIEGISGAWKRREDESKSAKIVSTIGASEGENKRQKIDEVCDGKAEAESLGTET
EQKKQQMEPTKDYIHVRARRGQATDSHSLAERARREKISERMKILQDLVPGCNKVIGKAL
VLDEIINYIQSLQRQVEFLSMKLEAVNSRMNPGIEVFPPKEVMILMIINSIFSIFFTKQY
MFLSRYSRGRSLDVYAVRSFKHCNKRSDLCFCSCSPKTELKTTIFSQNMTCFCRYSRVGV
AISSSKHCNEPFGQQAFENPEIQFGSQSTREYSRGASPEWLHMQIGSGGFERTS*
>G2533 (1..1080)
ATGATAAGCAAGGATCCAATATCGAGTTTACCTCCAGGGTTTCGATTTCATCCAACAGAT
GAAGAACTCATTCTCCATTACCTAAGGAAGAAAGTTTCCTCTTCCCCAGTCCCGCTTTCG
ATTATCGCCGATGTCGATATCTACAAATCCGATCCATGGGATTTACCAGCTAAGGCTCCA
TTTGGGGAGAAAGAGTGGTATTTTTTCAGTCCGAGGGATAGGAAATATCCAAACGGAGCA
AGACCAAACAGAGCAGCTGCGTCTGGATATTGGAAAGCAACCGGAACAGATAAATTGATT
GCGGTACCAAATGGTGAAGGGTTTCATGAAAACATTGGTATAAAAAAAGCTCTTGTGTTT
TATAGAGGAAAGCCGTCCAAAAGGTGTTAAAACCAATTGGATCATGCATGAATATCGTCTT
GCCGATTCATTATCTCCCAAAAGAATTAACTCTTCTAGGAGCGGTGGTAGCGAAGTTAAT
AATAATTTTGGAGATAGGAATTCTAAAGAATATTCGATGAGACTGGATGATTGGGTTCTT
TGCCGGATTTACAAGAAATCACACGCTTCATTGTCATCACCTGATGTTGCTTTGGTCACA
AGCAATCAAGAGCATGAGGAAAATGACAACGAACCATTCGTAGACCGCGGAACCTTTTTG
CCAAATTTGCAAAATGATCAACCCCTTAAACGCCAGAAGTCTTCTTGTTCGTTCTCAAAC
TTACTAGACGCTACAGATTTGACGTTTCTCGCAAATTTTCTAAACGAAACCCCGGAAAAT
CGTTCTGAATCAGATTTTTCTTTCATGATTGGCAATTTCTCTAATCCTGACATTTACGGA
AACCATTACTTGGATCAGAAGTTACCGCAGTTGAGCTCTCCCACTTCAGAGACAAGCGGC
ATCGGAAGCAAAAGAGAGAGAGTGGATTTTGCGGAAGAAACGATAAACGCTTCGAAGAAG

ATGATGAACACATATAGTTACAATAATAGTATAGATCAAATGGATCATAGTATGATGCAA
CAACCTAGTTTCCTGAACCAGGAACTCATGATGAGTTCTCACCTTCAATATCAAGGCTAG
>G2533 Amino Acid Sequence (conserved domain in AA coordinates:11-186)
MISKDPISSLPPGFRFHPTDEELILHYLRKKVSSSPVPLSIIADVDIYKSDPWDLPAKAP
FGEKEWYFFSPRDRKYPNGARPNRAAASGYWKATGTDKLIAVPNGEGFHENIGIKKALVF
YRGKPPKGVKTNWIMHEYRLADSLSPKRINSSRSGGSEVNNNFGDRNSKEYSMRLDDWVL
CRIYKKSHASLSSPDVALVTSNQEHEENDNEPFVDRGTFLPNLQNDQPLKRQKSSCSFSN
LLDATDLTFLANFLNETPENRSESDFSFMIGNFSNPDIYGNHYLDQKLPQLSSPTSETSG
IGSKRERVDFAEETINASKKMMNTYSYNNSIDQMDHSMMQQPSFLNQELMMSSHLQYQG*
>G2534 (1..975)
ATGGATAATATAATGCAATCGTCAATGCCACCGGGATTCCGATTTCATCCGACAGAGGAA
GAGCTTGTGGGTTATTACCTAGATAGGAAGATCAATTCAATGAAGAGTGCTTTAGATGTC
ATTGTAGAGATTGATCTCTACAAAATGGAGCCATGGGATATACAAGCGAGGTGTAAACTA
GGGTATGAAGAGCAAAACGAGTGGTACTTCTTTAGTCATAAGGACAGGAAGTACCCTACC
GGGACTAGGACCAACCGAGCCACTGCGGCTGGGTTCTGGAAAGCCACGGGTAGAGACAAG
GCGGTACTATCAAAAAACAGTGTCATCGGAATGCGGAAGACACTTGTCTACTACAAGGGT
CGAGCTCCTAATGGAAGAAAGTCCGATTGGATCATGCACGAATACCGTCTCCAAAACTCC
GAGCTTGCCCCGGTTCAGGAGGAAGGCTGGGTGGTGTGTCGAGCATTTAGGAAGCCAATT
CCAAACCAGAGGCCATTAGGGTACGAGCCATGGCAGAACCAGCTCTACCACGTCGAAAGT
AGTAACAACTACTCATCTTCAGTGACAATGAACACGAGTCATCATATCGGTGCATCTTCA
TCAAGTCATAACCTTAATCAAATGCTCATGAGCAATAACCACTACAATCCTAATAATACA
TCCTCATCGATGCATCAATATGGCAACATTGAGCTCCCGCAGTTGGACAGCCCGAGCTTG
TCGCCTAGTTTAGGGACGAATAAAGATCAGAACGAGAGTTTCGAGCAAGAAGAAGAGAAG
AGCTTTAACTGTGTGGATTGGAGAACACTAGATACCTTGCTTGAGACACAAGTCATACAT
CCGCATAACCCTAATATTCTTATGTTCGAAACGCAGTCGTATAATCCGGCGCCAAGCTTC
CCTTCCATGCATCAAAGCTATAATGAGGTCGAAGCTAATATTCATCATTCTCTTGGATGC
TTCCCTGACTCGTAA
>G2534 Amino Acid Sequence (conserved domain in AA coordinates:10-157)
MDNIMQSSMPPGFRFHPTEEELVGYYLDRKINSMKSALDVIVEIDLYKMEPWDIQARCKL
GYEEQNEWYFFSHKDRKYPTGTRTNRATAAGFWKATGRDKAVLSKNSVIGMRKTLVYYKG
RAPNGRKSDWIMHEYRLQNSELAPVQEEGWVVCRAFRKPIPNQRPLGYEPWQNQLYHVES
SNNYSSSVTMNTSHHIGASSSSHNLNQMLMSNNHYNPNNTSSSMHQYGNIELPQLDSPSL
SPSLGTNKDQNESFEQEEEKSFNCVDWRTLDTLLETQVIHPHNPNILMFETQSYNPAPSF
PSMHQSYNEVEANIHHSLGCFPDS*
>G2573 (34..957)
CCAGATTTAATTTGAGACTCTCAAAGAAACACCATGGAAGAAGAGCAACCTCCGGCCAAG
AAACGAAACATGGGGAGATCTAGAAAAGGTTGCATGAAAGGTAAAGGCGGTCCAGAGAAC
GCCACGTGTACTTTCCGTGGAGTTAGGCAACGGACTTGGGGTAAATGGGTGGCTGAGATC
CGTGAGCCTAACCGTGGGACTCGTCTCTGGCTCGGCACGTTTAATACCTCGGTCGAGGCC
GCCATGGCTTACGATGAAGCCGCTAAGAAACTCTATGGACACGAGGCTAAACTCAACTTG
GTGCACCCACAACAACAACAACAAGTAGTAGTGAACAGAAACTTGTCTTTTTCTGGCCAC
GGGTCGGGTTCTTGGGCTTATAATAAGAAGCTCGATATGGTTCATGGGTTGGACCTTGGT
CTCGGCCAGGCAAGTTGTTCACGAGGTTCTTGCTCAGAGAGATCGAGTTTTCTACAAGAA
GATGATGATCATAGTCATAATCGATGTTCGTCTTCAAGTGGTTCGAATCTTTGTTGGTTA
TTACCTAAACAAAGTGATTCACAAGATCAAGAGACCGTTAATGCTACGACTAGTTATGGC
GGTGAAGGCGGTGGTGGCTCTACGTTAACGTTTTCGACCAATTTGAAACCAAAGAATTTG
ATGAGTCAGAATTATGGATTATACAATGGAGCTTGGTCTAGGTTTCTTGTGGGGCAAGAA
AAGAAGACGGAACATGACGTGTCATCGTCGTGTGGATCGTCGGACAACAAGGAGAGTATG
TTGGTTCCTAGTTGCGGCGGAGAGAGGATGCATAGGCCGGAGTTGGAAGAGCGAACAGGA
TATTTGGAAATGGATGATCTTTTGGAGATTGATGATTTAGGTTTGTTGATTGGCAAAAAT
GGAGATTTCAAGAATTGGTGTTGTGAAGAGTTTCAACATCCATGGAATTGGTTCTGAGAG
TTTTTATTTATTACTATTATTTATCATACATATTTCTTATATTTGACTTAGG
>G2573 Amino Acid Sequence (domain in AA coordinates: TBD)
MEEEQPPAKKRNMGRSRKGCMKGKGGPENATCTFRGVRQRTWGKWVAEIREPNRGTRLWL
GTFNTSVEAAMAYDEAAKKLYGHEAKLNLVHPQQQQQVVVNRNLSFSGHGSGSWAYNKKL
DMVHGLDLGLGQASCSRGSCSERSSFLQEDDDHSNRCSSSSGSNLCWLLPKQSDSQDQE
TVNATTSYGGEGGGGSTLTFSTNLKPKNLMSQNYGLYNGAWSRFLVGQEKKTEHDVSSSC

GSSDNKESMLVPSCGGERMHRPELEERTGYLEMDDLLEIDDLGLLIGKNGDFKNWCCEEF
QHPWNWF*
>G2589 (23..1354)
AAAGAAAAGAAAAATAAAGATAATGAGGACGAAGACTAAGTTAGTACTCATACCTGATAG
ACACTTTCGGAGAGCCACATTCAGGAAGAGGAATGCAGGGATAAGGAAGAAACTCCACGA
GCTGACAACTCTCTGTGACATCAAAGCATGTGCGGTAATCTACAGTCCGTTCGAGAATCC
AACGGTGTGGCCGTCAACCGAAGGTGTTCAAGAGGTGATTTCGGAGTTCATGGAGAAGCC
GGCGACAGAACGGTCCAAGACGATGATGAGTCATGAGACTTTCTTGCGGGACCAAATCAC
CAAAGAACAAAACAAACTAGAGAGTCTACGTCGTGAAAACCGAGAAACTCAGCTTAAGCA
TTTTATGTTTGATTGCGTTGGAGGCAAGATGAGTGAGCAACAGTATGGTGCAAGGGACCT
TCAAGATTTAAGTCTTTTTACTGATCAATATCTTAATCAGCTTAATGCCAGGAAGAAGTT
CCTTACAGAATATGGTGAGTCTTCTTCTTCTGTTCCTCCTCTGTTTGATGTTGCGGGTGC
CAATCCTCCTGTTGTTGCAGATCAAGCTGCGGTAACTGTTCCTCCTTTGTTTGCTGTTGC
GGGTGCCAATCTTCCTGTTGTTGCTGATCAAGCTGCGGTAACTGTTCCTCCTCTGTTTGC
TGTTGCGGGTGCCAATCTTCCTGTTGTTGCAGATCAAGCTGCGGTTAATGTTCCTACTGG
ATTTCATAACATGAATGTGAACCAGAATCAGTATGAGCCGGTTCAGCCCTATGTCCCTAC
TGGTTTTAGTGATCATATTCAATATCAGAATATGAACTTCAATCAAAACCAACAAGAGCC
GGTTCATTACCAGGCTCTTGCTGTTGCGGGTGCCGGTCTTCCTATGACTCAGAATCAGTA
TGAGCCCGTTCACTACCAGAGTCTTGCTGTCGCGGGTGGCGGTCTTCCTATGAGTCAGTT
GCAGTATGAGCCGGTTCAGCCTTATATCCCTACTGTTTTTAGTGATAATGTTCAATATCA
GCATATGAATTTGTATCAAAATCAACAAGAGCCGGTTCACTACCAAGCTCTTGGTGTTGC
AGGTGCCGGTCTTCCTATGAATCAGAATCAGTATGAGCCGGTTCAGCCCTATGTCCCTAC
TGGTTTTAGTGATCATTTTCAGTTTGAGAATATGAATTTGAATCAAAATCAACAGGAGCC
GGTTCAATACCAAGCTCCTGTTGATTTTAATCATCAGATTCAACAAGGAAACTATGATAT
GAATTTGAACCAGAATATGAGTTTGGATCCAAATCAGTATCCGTTTCAAAATGATCCATT
CATGAATATGTTGACAGAATATCCTTATGAATAAGCGGGTTATGTTGGAGAGCATGCAC
>G2589 Amino Acid Sequence (domain in AA coordinates: TBD)
MRTKTKLVLIPDRHFRRATFRKRNAGIRKKLHELTTLCDIKACAVIYSPFENPTVWPSTE
GVQEVISEFMEKPATERSKTMMSHETFLRDQITKEQNKLESLRRENRETQLKHFMFDCVG
GKMSEQQYGARDLQDLSLFTDQYLNQLNARKKFLTEYGESSSSVPPLFDVAGANPPVVAD
QAAVTVPPLFAVAGANLPVVADQAAVTVPPLFAVAGANLPVVADQAAVNVPTGFHNMNVN
QNQYEPVQPYVPTGFSDHIQYQNMNFNQNQQEPVHYQALAVAGAGLPMTQNQYEPVHYQS
LAVAGGGLPMSQLQYEPVQPYIPTVFSDNVQYQHMNLYQNQQEPVHYQALGVAGAGLPMN
QNQYEPVQPYVPTGFSDHFQFENMNLNQNQQEPVQYQAPVDFNHQIQQGNYDMNLNQNMS
LDPNQYPFQNDPFMNMLTEYPYE*
>G2687 (45..1139)
CTCTGTCTCTCGTATCTTTCTACTACTCTGTTTCTTGAATTCTAATGAACAACATCGACG
ACGCAAAGACGGAGACTTCAGTGTCTTCAGGTTCAAGCGACTCTTTCTTGCCTCTCAAGA
AACGCATGAGACTTGATGACGAACCAGAAAACGCCCTAGTGGTTTCGTCTTCACCAAAGA
CGGTTGTGGCTTCTGGCAATGTCAAGTACAAAGGAGTCGTTCAGCAACAGAACGGTCATT
GGGGTGCCCAGATTTACGCAGACCACAAAAGGATTTGGCTTGGAACTTTCAAATCCGCTG
ATGAAGCCGCCACGGCTTACGATAGTGCATCTATCAAACTCCGAAGCTTTGACGCTAACT
CGCACCGGAACTTCCCTTGGTCTACAATCACTCTCAACGAACCAGACTTTCAAAATTGCT
ACACAACAGAGACTGTGTTGAACATGATCAGAGACGGTTCGTACCAACACAAATTCAGAG
ATTTTCTCAGAATCAGATCTCAGATTGTTGCGAGTATCAACATCGGGGGACCAAAACAAG
CCCGAGGAGAAGTGAATCAAGAATCAGACAAGTGTTTTTCTTGCACACAGCTTTTTCAGA
AGGAATTGACACCGAGCGATGTAGGGAAACTAAATAGGCTTGTGATACCTAAAAAGTATG
CAGTGAAGTATATGGCTTTCATAAGCGCTGATCAAAGCGAGAAAGAAGAGGGTGAAATAG
TAGGATCTGTGGAAGATGTGGAGGTTGTGTTTTACGACAGAGCAATGAGACAATGGAAGT
TTAGGTATTGTTACTGGAAAAGTAGCCAGAGCTTTGTCTTCACCAGAGGATGGAATAGTT
TCGTGAAGGAGAAGAATCTCAAGGAGAAGGATGTTATTGCCTTCTACACTTGCGATGTCC
CGAACAATGTGAAGACATTAGAAGGTCAAAGAAAGAACTTCTTGATGATCGATGTTCATT
GCTTTTCAGACAACGGTTCCGTGGTAGCTGAGGAAGTAAGTATGACGGTTCATGACAGTT
CAGTGCAAGTAAAGAAAACAGAAAACTTGGTTAGCTCCATGTTAGAAGATAAAGAAACCA
AATCAGAGGAGAACAAAGGAGGGTTTATGCTGTTTGGTGTAAGGATCGAATGTCCTTAGG
GAATTTTTCTTTAAAAGTTTCTTACTTCAACTAGAACTTGTTTTACTTGTACCT
>G2687 Amino Acid Sequence (domain in AA coordinates: TBD)

MNNIDDAKTETSVSSGSSDSFLPLKKRMRLDDEPENALVVSSSPKTVVASGNVKYKGVVQ
QQNGHWGAQIYADHKRIWLGTFKSADEAATAYDSASIKLRSFDANSHRNFPWSTITLNEP
DFQNCYTTETVLNMIRDGSYQHKFRDFLRIRSQIVASINIGGPKQARGEVNQESDKCFSC
TQLFQKELTPSDVGKLNRLVIPKKYAVKYMPFISADQSEKEEGEIVGSVEDVEVVFYDRA
MRQWKFRYCYWKSSQSFVFTRGWNSFVKEKNLKEKDVIAFYTCDVPNNVKTLEGQRKNFL
MIDVHCFSDNGSVVAEEVSMTVHDSSVQVKKTENLVSSMLEDKETKSEENKGGFMLFGVR
IECP*

>G27 (83..622)

CAAAATACCAAAAACAAAACATTTTTTTTAATCTTCCCACCAATTTTTTTCTCTTTCTCT
CGTTACATTAAATTATCTTTAGATGCAAGACTCTTCCTCTCACGAATCGCAACGTAACCT
CCGGTCACCGGTGCCGGAGAAAACCGGAAAGAGTTCTAAGACTAAAAATGAGCAAAAAGG
TGTTTCTAAACAACCAAATTTTCGTGGGGTCAGAATGAGACAATGGGGAAAATGGGTGTC
TGAAATTAGAGAACCAAGAAAGAAATCAAGAATATGGCTCGGTACTTTCTCTACGCCGGA
GATGGCGGCGCGTGCACACGACGTGGCGGCTTTAGCCATCAAAGGTGGCTCTGCCCACCT
TAATTTCCCGGAGCTAGCTTACCATTTGCCGAGACCGGCTAGCGCGGACCCTAAAGACAT
TCAAGAAGCCGCCGCCGCAGCAGCTGCCGTTGACTGGAAAGCACCGGAGTCTCCGTCTAG
CACCGTGACGTCATCTCCAGTCGCCGACGACGCTTTCTCCGATCTTCCTGATCTTTTGCT
TGACGTGAATGATCACAACAAAAACGATGGATTCTGGGACTCGTTTCCGTACGAAGATCC
TTTCTTCTTGGAAAATTACTAGAAGGCAAATTCTTGCCGGCGAACGGATTTTCCGGTGGT
TTCCCGGTAAATAAGAAGACGATGTCGTTTTGTACCTTTTTTGTCTACGATGGGAAATTT
CTTTTTTTTTTACGTGTGAGTAAAAGTTTCCGAATGTGTGATGTGTAAGTAAGTACAGGT
TATTTAATTTCTTTTTTTTGTACAAATACGTACGTCATTACCAAAAAGTTTTCATTTATT
GTGCTTTTATCTTCCAAATTCATTAAAAAAAAAAAAAAAAA

>G27 Amino Acid Sequence (domain in AA coordinates: 37-104)

MQDSSSHESQRNLRSPVPEKTGKSSKTKNEQKGVSKQPNFRGVRMRQWGKWVSEIREPRK
KSRIWLGTFSTPEMAARAHDVAALAIKGGSAHLNFPELAYHLPRPASADPKDIQEAAAAA
AAVDWKAPESPSSTVTSSPVADDAFSDLPDLLLDVNDHNKNDGFWDSFPYEDPFFLENY*

>G2720 (1..894)

ATGGAAGCGAAGAAGGAAGAGATAAAGAAAGGTCCATGGAAAGCCGAAGAAGACGAAGTA
CTCATCAACCATGTCAAGAGATACGGTCCTCGTGATTGGAGCTCCATTCGATCCAAAGGT
CTTCTTCAACGCACCGGCAAATCCTGTCGTCTTCGTTGGGTCAATAAACTCCGTCCCAAT
CTCAAAAATGGATGCAAGTTCTCGGCTGACGAAGAGAGGACTGTGATTGAGTTACAATCT
GAGTTTGGTAACAAATGGGCGAGAATCGCTACGTATCTACCGGGAAGAACTGATAACGAT
GTGAAGAATTTCTGGAGTAGCAGACAAAAGAGACTCGCTAGGATTCTTCATAACTCCTCT
GATGCATCGAGTTCGAGTTTCAATCCCAAATCTTCTTCTTCTCATCGACTCAAGGGCAAA
AACGTCAAACCAATCCGTCAATCCTCTCAGGGTTTTGGTTTGGTTGAGGAAGAGGTTACA
GTTTCTTCTTCATGTTCCCAGATGGTTCCTTATTCATCTGATCAAGTTGGTGATGAAGTC
TTGAGGTTGCCGGATTTGGGTGTTAAGTTAGAGCATCAGCCTTTCGCTTTTGGCACTGAT
CTTGTCCTAGCAGAGTACTCTGACTCACAGAATGATGCAAATCAGCAAGCAATCAGCCCT
TTCTCTCCAGAAAGCAGAGAGCTTTTGGCTAGACTTGACGACCCTTTTTACTATGATATA
CTTGGACCAGCTGATTCTTCTGAGCCATTGTTCGCTCTCCCTCAGCCGTTCTTCGAGCCT
TCGCCTGTGCCGAGAAGATGCAGACATGTTTCAAAGGATGAAGAAGCTGATGTTTTCTTA
GACGATTTCCCAGCTGACATGTTTGATCAGGTTGATCCAATCCCAAGTCCTTAG

>G2720 Amino Acid Sequence (domain in AA coordinates: 10-114)

MEAKKEEIKKGPWKAEEDEVLINHVKRYGPRDWSSIRSKGLLQRTGKSCRLRWVNKLRPN
LKNGCKFSADEERTVIELQSEFGNKWARIATYLPGRTDNDVKNFWSSRQKRLARILHNSS
DASSSSFNPKSSSSHRLKGKNVKPIRQSSQGFGLVEEEVTVSSSCSQMVPYSSDQVGDEV
LRLPDLGVKLEHQPFAFGTDLVLAEYSDSQNDANQQAISPFSPESRELLARLDDPFYYDI
LGPADSSEPLFALPQPFFEPSPVPRRCRHVSKDEEADVFLDDFPADMFDQVDPIPSP*

>G2787 (142..1584)

TCTCAGAGCAAAAAACAAAAAAAAAGAAAAAAAAACCCTAAATCTAAATCTCACCTTCCA
CCTCTGTCTTTTTTTTTTTTTGTTCTTTTTTTTTTTTTTTACTGTATCTTCTCTTCTCTTTG
CTCTGCAAAAATCTCACATCCATGGATCCATCTCTTGGTGATCCTCATCATCCTCCTCAG
TTCACCCCTTTTCCTCATTTTCCCACCTCCAATCATCATCCTTTAGGACCAAATCCGTAC
AATAACCATGTCGTCTTCCAACCGCAGCCGCAAACGCAAACGCAAATCCCGCAACCGCAG
ATGTTTCAGTTATCTCCACATGTTTCAATGCCCCACCCTCCTTACTCCGAAATGATTTGC
GCTGCGATTGCGGCGTTAAACGAACCGGATGGTTCGAGCAAGATGGCAATTTCGAGATAC

ATCGAGAGATGTTACACCGGTTTAACTTCTGCTCATGCTGCTTTGTTGACTCACCATCTC
AAGACTTTGAAGACCAGTGGTGTTCTTTCTATGGTTAAGAAATCTTACAAAATTGCTGGT
TCTTCTACTCCTCCTGCTAGTGTAGCTGTTGCTGCTGCTGCCGCCGCTCAAGGTCTCGAT
GTTCCCAGATCTGAGATTCTCCATTCAAGTAACAACGATCCCATGGCTTCTGGCTCTGCT
TCTCAGCCTCTGAAACGAGGTCGTGGTCGTCCTCCTAAGCCTAAACCTGAATCTCAACCA
CAACCACTACAGCAACTTCCACCGACCAATCAAGTCCAGGCTAACGGACAGCCAATCTGG
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AGAGGACCTGGTCGTCCAAGGAAGAACGGTTCTGCTGCTCCTGCTACTGCACCAATCGTT
CAAGCTTCGGTTATGGCTGGAATTATGAAACGTAGAGGTAGACCACCGGGTCGTCGAGCT
GCTGGGAGACAGAGGAAGCCCAAATCCGTTTCTTCTACTGCCTCTGTGTATCCTTATGTT
GCTAATGGTGCTAGACGCAGAGGAAGGCCTAGGAGAGTTGTTGACCCTAGCAGTATTGTT
AGTGTTGCTCCAGTAGGTGGTGAAAATGTGGCAGCGGTTGCGCCAGGGATGAAGCGTGGA
CGTGGACGACCACCTAAGATTGGTGGTGTTATCAGTAGGCTTATTATGAAGCCTAAGAGA
GGACGAGGACGTCCTGTAGGTAGACCCAGAAAGATTGGAACATCAGTCACGACTGGGACA
CAAGATTCTGGAGAACTCAAGAAGAAGTTTGATATTTTTCAAGAGAAAGTGAAAGAAATT
GTGAAGGTGTTGAAGGATGGAGTTACAAGTGAGAATCAAGCAGTGGTGCAAGCCATAAAA
GATCTGGAAGCACTAACAGTGACGGAGACCGTTGAGCCACAAGTTATGGAAGAAGTGCAG
CCAGAGGAGACTGCAGCACCACAGACTGAAGCTCAACAAACTGAAGCTGCTGAGACACAA
GGAGGACAAGAAGAAGGACAAGAAAGAGAAGGAGAAACACAGACCCAGACACAGAAGCAGAG
GCAATGCAAGAAGCTCTGTTCTGAAGAATAATAATGATCTAGAAAACAACCTAGACATAA
TAGCCTTGGTGTTTGGCGTTAGGAGTGTTTTTTTTTAGTTGTTTTAGGTGTTGGAATCGC
ATCTTAAATTATATAAAAATCTATAAGGAATTTTAATTTTTCTAGGTTTTGTTGTCTGCA
GAAGAAGAAATAGTAGACTCGTTAATGGTGTTGTTGTCGGTGTGTCTTTAACCAAACCAT
AAGACGTGGCTGTAAATTAGCGATGTTTCTAGTCTTCCATCTTTAATAATCTCTTATTGC
GTCTGTGCCTTTGTTTTT

>G2787 Amino Acid Sequence (domain in AA coordinates: 172-192, 226-247, 256-276, 290-311, 245-366)
MDPSLGDPHHPPQFTPFPHFPTSNHHPLGPNPYNNHVVFQPQPQTQTQIPQPQMFQLSPH
VSMPHPPYSEMICAAIAALNEPDGSSKMAISRYIERCYTGLTSAHAALLTHHLKTLKTSG
VLSMVKKSYKIAGSSTPPASVAVAAAAAAQGLDVPRSEILHSSNNDPMASGSASQPLKRG
RGRPPKPKPESQPQPLQQLPPTNQVQANGQPIWEQQQVQSPVPVPTPVTESAKRGPGRPR
KNGSAAPATAPIVQASVMAGIMKRRGRPPGRRAAGRQRKPKSVSSTASVYPYVANGARRR
GRPRRVVDPSSIVSVAPVGGENVAAVAPGMKRGRGRPPKIGGVISRLIMKPKRGRGRPVG
RPRKIGTSVTTGTQDSGELKKKFDIFQEKVKEIVKVLKDGVTSENQAVVQAIKDLEALTV
TETVEPQVMEEVQPEETAAPQTEAQQTEAAETQGGQEEGQEREGETQTQTEAEAMQEALF
*

>G2789 (82..879)
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TTTTAGCGAATCAGAAGAGGAATGGATGAGGTATCTCGTTCTCATACACCGCAATTTCTA
TCAAGTGATCATCAGCACTATCACCATCAAAACGCTGGACGACAAAAACGCGGCAGAGAA
GAAGAAGGAGTTGAACCCAACAATATAGGGGAAGACCTAGCCACCTTTCCTTCCGGAGAA
GAGAATATCAAGAAGAGAAGGCCACGTGGCAGACCTGCTGGTTCCAAGAACAAACCCAAA
GCACCAATCATAGTCACTCGCGACTCCGCGAACGCCTTCAGATGTCACGTCATGGAGATA
ACCAACGCCTGCGATGTAATGGAAAGCCTAGCCGTCTTCGCTAGACGCCGTCAGCGTGGC
GTTTGCGTCTTGACCGGAAACGGGGCCGTTACAAACGTCACCGTTAGACAACCTGGCGGA
GGCGTCGTCAGTTTACACGGACGGTTTGAGATTCTTTCTCTCTCGGGTTCGTTTCTTCCT
CCACCGGCACCACCAGCTGCGTCTGGTTTAAAGGTTTACTTAGCCGGTGGTCAAGGTCAA
GTGATCGGAGGCAGTGTGGTGGGACCGCTTACGGCATCAAGTCCGGTGGTCGTTATGGCA
GCTTCATTTGGAAACGCATCTTACGAGAGGCTGCCACTAGAGGAGGAGGAGGAAACTGAA
AGAGAAATAGATGGAAACGCGGCTAGGGCGATTGGAACGCAAACGCAGAAACAGTTAATG
CAAGATGCGACATCGTTTATTGGGTCGCCGTCGAATTTAATTAACTCTGTTTCGTTGCCA
GGTGAAGCTTATTGGGGAACGCAACGACCGTCTTTCTAAGATAATATCATTGATAATATA
AGTTTCGTCTTCTTATTCTTTTTCACTTTTTACCTTTTTCACTTTCTTAGGTTTTGTTTT
AACGTTTGATTAATACCTGAAGGTTTTTGGAAAATTTTCGATCGGATAAAAGGATTTATG
TTGCGAGCCGAAACGCGGCC

>G2789 Amino Acid Sequence (domain in AA coordinates: 53-73, 121-165)
MDEVSRSHTPQFLSSDHQHYHHQNAGRQKRGREEEGVEPNNIGEDLATFPSGEENIKKRR

PRGRPAGSKNKPKAPIIVTRDSANAFRCHVMEITNACDVMESLAVFARRRQRGVCVLTGN
GAVTNVTVRQPGGGVVSLHGRFEILSLSGSFLPPPAPPAASGLKVYLAGGQGQVIGGSVV
GPLTASSPVVVMAASFGNASYERLPLEEEEETEREIDGNAARAIGTQTQKQLMQDATSFI
GSPSNLINSVSLPGEAYWGTQRPSF*
>G31 (13..615)
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GGCGGAGGGAAGACGATGACGATGACGACGATGCGGAAGGAAGTGCACTTTAGAGGTGTG
AGGAAGCGTCCATGGGGTAGATACGCGGCGGAGATCCGTGACCCGGGAAAGAAAACCCGG
GTTTGGCTCGGGACATTCGACACGGCGGAGGAAGCTGCAAGAGCTTACGACACCGCCGCT
AGAGAGTTTCGTGGCTCCAAAGCAAAGACTAATTTCCCTCTTCCCGGAGAGTCTACTACG
GTTAACGACGGTGGCGAGAACGATTCTTACGTCAACCGTACGACGGTGACGACGGCGCGT
GAGATGACGCGTCAGAGATTTCCGTTTGCATGTCACCGGGAGCGTAAAGTCGTCGGTGGT
TATGCTTCTGCTGGTTTTTTCTTCGATCCGTCAAGAGCTGCTTCGTTAAGAGCAGAGCTT
TCTCGGGTTTGTCCGGTTCGGTTTGATCCGGTTAATATCGAGTTGAGTATTGGTATTCGA
GAAACCGTAAAAGTTGAACCGAGAAGAGAACTAAACCTGGATCTTAACCTAGCTCCACCG
GTGGTGGACGTTTAGATTTTTTTCTTCTTTTCATAATTTGTATTTTACATTGCCGGAAAA
TAATTAATGTTTTCTTTAG
>G31 Amino Acid Sequence (domain in AA coordinates: TBD)
MAPRQANGRSIAVSEGGGGKTMTMTTMRKEVHFRGVRKRPWGRYAAEIRDPGKKTRVWLG
TFDTAEEAARAYDTAAREFRGSKAKTNFPLPGESTTVNDGGENDSYVNRTTVTTAREMTR
QRFPFACHRERKVVGGYASAGFFFDPSRAASLRAELSRVCPVRFDPVNIELSIGIRETVK
VEPRRELNLDLNLAPPVVDV*
>G33 (20..757)
ATTCTCCCCCAACCAAAATATGACCACAGAAAAAGAGAATGTCACTACGGCCGTGGCCGT
GAAAGACGGCGGAGAAAAGAGTAAGGAAGTGAGTGACAAGGGCGTAAAGAAGAGAAAGAA
TGTAACTAAGGCCCTGGCCGTGAATGACGGCGGAGAAAAGAGTAAGGAAGTGCGTTACAG
GGGTGTAAGGAGGAGACCATGGGGGAGATATGCTGCGGAGATCCGTGATCCGGTAAAGAA
AAAACGGGTCTGGCTCGGGTCCTTCAACACGGGGGAGGAAGCCGCCAGAGCCTACGACTC
CGCTGCCATAAGGTTTCGAGGATCGAAAGCTACTACTAACTTCCCTCTAATCGGATACTA
TGGGATTTCTTCGGCGACGCCGGTGAACAACAACCTTTCCGAGACGGTGAGTGATGGAAA
TGCCAACCTCCCTCTCGTTGGAGACGATGGGAATGCTTTGGCTTCTCCGGTGAACAACAC
CCTTTCCGAAACGGCGCGTGATGGAACACTTCCATCGGATTGTCACGACATGTTATCTCC
GGGGGTGGCTGAAGCGGTTGCTGGATTTTTCTTAGATCTGCCTGAAGTTATTGCGTTGAA
AGAGGAGCTTGATCGAGTTTGTCCTGACCAGTTTGAGTCCATTGATATGGGGTTGACTAT
TGGTCCTCAAACCGCCGTGGAAGAGCCTGAGACTTCCTCCGCCGTGGATTGTAAGCTGCG
AATGGAACCGGATCTTGACCTCAACGCAAGTCCCTAAAGATTGATCTGATGTTGTTGTCC
TTGAATAAGTTTGTTATCTTGTCGCTCTTCTGATTGTCTGTACTTCTATTGGTTGATTCG
TGCTTTTGGAGGACAAAACAAACATTTTTTTATGTATTAAAAAAAGGTAATTGAACTATT
ATCGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
>G33 Amino Acid Sequence (domain in AA coordinates: 50-117)
MTTEKENVTTAVAVKDGGEKSKEVSDKGVKKRKNVTKALAVNDGGEKSKEVRYRGVRRRP
WGRYAAEIRDPVKKKRVWLGSFNTGEEAARAYDSAAIRFRGSKATTNFPLIGYYGISSAT
PVNNNLSETVSDGNANLPLVGDDGNALASPVNNTLSETARDGTLPSDCHDMLSPGVAEAV
AGFFLDLPEVIALKEELDRVCPDQFESIDMGLTIGPQTAVEEPETSSAVDCKLRMEPDLD
LNASP*
>G342 (1..723)
ATGGACGTCTACGGCATGTCTTCACCGGACTTGCTTCGTATCGACGACCTTCTCGATTTC
TCCAACGACGAAATCGTTCTCTTCCTCTTCCACCGTCACTTCCTCCGCCGCTTCCTCCGCC
GCTTCTTCCGAAAACCCTTTCAGCTTTCCTTCTTCCACCTACACTTCTCCTACTCTCCTC
ACCGACTTCACTCACGATCTCTGCGTTCCCAGTGACGACGCAGCTCATCTCGAATGGTTA
TCGCGATTCGTTGACGATTCATTCTCCGATTTCCCAGCAAATCCTTTAACCATGACCGTT
AGACCCGAGATTTCATTCACCGGAAAACCTAGAAGTCGCCGATCAAGAGCACCAGCACCT
TCCGTAGCTGGAACTTGGGCTCCGATGTCTGAATCAGAGCTTTGTCACTCCGTCGCTAAA
CCTAAACCGAAGAAAGTCTACAACGCTGAATCGGTTACGGCGGATGGAGCGAGGCGGTGC
ACGCACTGTGCCTCGGAGAAAACGCCACAGTGGAGAACTGGACCGCTTGGACCTAAAACA
CTTTGTAACGCTTGTGGAGTTCGTTACAAATCAGGGAGGCTTGTACCGGAATACAGACCG
GCGTCGAGTCCGACGTTTGTATTGACTCAGCATTCGAACTCTCATCGGAAAGTTATGGAG

CTCCGGCGACAGAAGGAACAACAAGAATCTTGCGTTCGAATTCCGCCGTTTCAGCCGCAG
TAA
>G342 Amino Acid Sequence (domain in AA coordinates: 155-190)
MDVYGMSSPDLLRIDDLLDFSNDEIFSSSSTVTSSAASSAASSENPFSFPSSTYTSPTLL
TDFTHDLCVPSDDAAHLEWLSRFVDDSFSDFPANPLTMTVRPEISFTGKPRSRRSRAPAP
SVAGTWAPMSESELCHSVAKPKPKKVYNAESVTADGARRCTHCASEKTPQWRTGPLGPKT
LCNACGVRYKSGRLVPEYRPASSPTFVLTQHSNSHRKVMELRRQKEQQESCVRIPPFQPQ
*
>G352 (80..817)
AATACACCACACACTTCACTCTTTCTTCATCTTCTTCTTCTTAAATAGCTCGAAATCACA
TCTCACAGAATTAAATCTTATGGCTCTCGAGACTCTCAATTCTCCAACAGCTACCACCAC
CGCTCGGCCTCTTCTCCGGTATCGTGAAGAAATGGAGCCTGAGAATCTCGAGCAATGGGC
TAAAAGAAAACGAACAAAACGTCAACGTTTTGATCACGGTCATCAGAATCAAGAAACGAA
CAAGAACCTTCCTTCTGAAGAAGAGTATCTCGCTCTTTGTCTCCTCATGCTCGCTCGTGG
CTCCGCCGTACAATCTCCTCCTCTTCCTCCTCTACCGTCACGTGCGTCACCGTCCGATCA
CCGAGATTACAAGTGTACGGTCTGTGGGAAGTCCTTTTCGTCATACCAAGCCTTAGGTGG
ACACAAGACGAGTCACCGGAAACCGACGAACACTAGTATCACTTCCGGTAACCAAGAACT
GTCTAATAACAGTCACAGTAACAGCGGTTCCGTTGTTATTAACGTTACCGTGAACACTGG
TAACGGTGTTAGTCAAAGCGGAAAGATTCACACTTGCTCAATCTGTTTCAAGTCGTTTGC
GTCTGGTCAAGCCTTAGGTGGACACAAACGGTGTCACTATGACGGTGGCAACAACGGTAA
CGGTAACGGAAGTAGCAGCAACAGCGTAGAACTCGTCGCTGGTAGTGACGTCAGCGATGT
TGATAATGAGAGATGGTCCGAAGAAAGTGCGATCGGTGGCCACCGTGGATTTGACCTAAA
CTTACCGGCTGATCAAGTCTCAGTGACGACTTCTTAA
>G352 Amino Acid Sequence (domain in AA coordinates: 99-119,166-186)
MALETLNSPTATTTARPLLRYREEMEPENLEQWAKRKRTKRQRFDHGHQNQETNKNLPSE
EEYLALCLLMLARGSAVQSPPLPPLPSRASPSDHRDYKCTVCGKSFSSYQALGGHKTSHR
KPTNTSITSGNQELSNNSHSNSGSVVINVTVNTGNGVSQSGKIHTCSICFKSFASGQALG
GHKRCHYDGGNNGNGNGSSSNSVELVAGSDVSDVDNERWSEESAIGGHRGFDLNLPADQV
SVTTS*
>G357 (1..615)
ATGCAGAACAAACACAAATGCAAGCTCTGTTCCAAGAGTTTCTGTAATGGCAGAGCACTT
GGTGGTCACATGAAGTCTCACTTGGTCTCATCTCAGTCTTCAGCTCGGAAGAAACTAGGT
GACTCGGTCTATTCTTCTTCTTCCTCTTCCTCCGATGGTAAAGCGCTCGCCTACGGGTTA
CGAGAGAACCCGAGGAAGAGTTTCCGGGTCTTTAATCCGGATCCTGAGTCATCCACAATT
TACAACAGTGAGACAGAGACCGAACCTGAATCCGGAGACCCGGTTAAGAAACGGGTCAGA
GGAGATGTTTCAAAGAAGAAGAAGAAGAAGGCAAAGAGTAAGAGAGTGTTTGAGAACTCG
AAGAAGCAAAAGACAATTCACGAGTCACCAGAACCAGCGAGTTCTGTCTCTGATGGTTCT
CCTGAACAAGATTTAGCTATGTGCTTGATGATGCTGTCAAGAGATTCAAGGGAGCTCGAG
ATTAAACTGAAAAAACCGGAGGAAGAGAGGAAGCCGGAAAAAAGACATTTCCCTGAGCTC
CGTCGCTGTATGATAGATCTGAATCTTCCTCCGCCGCAAGAAGCTGAAGCTGTCACCGTC
GTTTCAGCCATATAA
>G357 Amino Acid Sequence (domain in AA coordinates: 7-29)
MQNKHKCKLCSKSFCNGRALGGHMKSHLVSSQSSARKKLGDSVYSSSSSSSDGKALAYGL
RENPRKSFRVFNPDPESSTIYNSETETEPESGDPVKKRVRGDVSKKKKKKAKSKRVFENS
KKQKTIHESPEPASSVSDGSPEQDLAMCLMMLSRDSRELEIKLKKPEEERKPEKRHFPEL
RRCMIDLNLPPPQEAEAVTVVSAI*
>G358 (1..855)
ATGGGTCAAGATGAGGTTGGGAGTGATCAGACGCAAATCATAAAAGGGAAACGTACGAAG
CGACAAAGATCGTCTTCGACGTTTGTGGTGACGGCGGCGACAACAGTGACTTCAACAAGT
TCATCGGCCGGTGGAAGTGGAGGAGAAAGAGCTGTTTCAGATGAATACAACTCGGCGGTT
TCGTCTCCGGTGACTACTGATTGTACGCAAGAAGAAGAAGACATGGCGATTTGTCTCATC
ATGTTAGCTCGTGGGACAGTTCTTCCATCGCCGGATCTCAAGAACTCGAGAAAAAATTCAT
CAGAAGATTTCGTCGGAGAATTCTAGTTTCTATGTGTACGAGTGTAAAACGTGTAACCGG
ACGTTTTCGTCGTTCCAAGCACTTGGTGGACACAGAGCGAGCCACAAGAAGCCGAGGACG
TCGACTGAGGAAAAGACTAGACTACCCCTGACGCAACCCAAGTCTAGTGCATCAGAAGAA
GGGCAAAACAGTCATTTCAAAGTTTCCGGCTCAGCCCTAGCTTCACAGGCAAGTAACATC
ATCAACAAGGCAAACAAAGTACACGAGTGTTCCATCTGCGGTTCTGAGTTCACTTCCGGG

CAAGCTCTCGGTGGTCACATGAGGCGGCACAGGACAGCCGTAACCACGATTAGCCCCGTT
GCAGCCACCGCAGAAGTAAGCAGAAACAGTACAGAGGAAGAGATTGAGATCAATATAGGC
CGTTCGATGGAACAGCAGAGGAAATATCTACCGTTGGATCTTAATCTACCAGCACCAGAA
GATGATCTAAGAGAGTCAAAGTTTCAAGGGATAGTATTCTCAGCAACACCAGCGTTAATA
GATTGTCATTACTAG
>G358 Amino Acid Sequence (domain in AA coordinates: 124-135, 188-210)
MGQDEVGSDQTQIIKGKRTKRQRSSSTFVVTAATTVTSTSSSAGGSGGERAVSDEYNSAV
SSPVTTDCTQEEEDMAICLIMLARGTVLPSPDLKNSRKIHQKISSENSSFYVYECKTCNR
TFSSFQALGGHRASHKKPRTSTEEKTRLPLTQPKSSASEEGQNSHFKVSGSALASQASNI
INKANKVHECSICGSEFTSGQALGGHMRRHRTAVTTISPVAATAEVSRNSTEEEIEINIG
RSMEQQRKYLPLDLNLPAPEDDLRESKFQGIVFSATPALIDCHY*
>G360 (1..543)
ATGTGGAACCCTAACAAAATTGAAGAATTGGAGGATGATGATGAATCTTGGGAAGTCAAA
GCCTTTGAGCAAGACACTAAAGGCAACATCTCTGGTACCACTTGGCCTCCAAGATCTTAC
ACTTGCAATTTCTGCCGCCGTGAGTTCCGTTCTGCTCAAGCCTTAGGCGGTCACATGAAT
GTCCACCGCCGTGACCGCGCCTCATCTAGGGCTCATCAAGGTTCCACCGTTGCGGCTGCG
GCTAGAAGCGGCCACGGGGGGATGTTACTCAATTCTTGTGCTCCGCCGTTGCCTACAACG
ACACTTATAATACAATCCACGGCGAGTAACATTGAAGGTTTGTCCCATTTCTACCAACTG
CAAAACCCTAGTGGCATTTTTGGTAATTCTGGTGACATGGTGAATCTTTATGTAGAAGTT
CCTCCTCGGCTTATTGAATATTCGACAGGAGATGATGAGAGCATTGGCTCGATGAAAGAA
GCGACAGGAACATCAGTGGATGAGCTTGATCTTGAACTTCGGCTAGGGCACCATCCACCG
TGA
>G360 Amino Acid Sequence (domain in aa coordinates: 42-62)
MWNPNKIEELEDDDESWEVKAFEQDTKGNISGTTWPPRSYTCNFCRREFRSAQALGGHMN
VHRRDRASSRAHQGSTVAAAARSGHGGMLLNSCAPPLPTTTLIIQSTASNIEGLSHFYQL
QNPSGIFGNSGDMVNLYVEVPPRLIEYSTGDDESIGSMKEATGTSVDELDLELRLGHHPP
*
>G362 (195..830)
ATAAAAAACCCTTCATACAATATAAAATTTCTTTAGACATACAATATATTATACTATTAC
AGATGCAATGCATCATTAGTTACAAACTATTAAACTAAATATCCCCCGTCTCTCTCTTGC
TATATAAAGAAGATCATTTACACATCTCCTTAAGCAAATTAAACCCATCGATAAACACAT
ACGTTCACACATATATGTCTATAAATCCGACAATGTCTCGTACTGGCGAAAGTTCTTCAG
GTTCGTCCTCCGACAAGACGATAAAGCTATTCGGCTTCGAACTCATCAGCGGCAGTCGTA
CGCCGGAAATCACGACGGCGGAAAGCGTGAGCTCGTCCACAAACACGACGTCGTTAACAG
TGATGAAAAGACACGAGTGCCAATACTGCGGTAAAGAGTTTGCAAATTCTCAAGCCTTAG
GAGGTCACCAAAACGCTCACAAGAAGGAGAGGTTGAAGAAGAAGAGGCTTCAGCTTCAAG
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ATCAGATGGGTGTGTACAACGAAGATTGGTCGTCGAGGTCGTCGCAGATTAACTTCGGTA
ATAATGACACGTGCCAAGATCTTAATGAACAAAGCGGTGAGATGGGTAAGCTGTACGGTG
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GTATTAACTCGCTGGATCTTCATCTAGGTTTTGCCGGAGATGCGGCATAACAAATTAAAG
AGAGATATATGATTAAGATTATATGTACTATAGTGGCGTATTTCATTGGGATCATGAAGG
GGAAAAAACGAGACATATAGTATTCTTGATGCAATTTGAGTTTTGTAATTTATTTAGGTT
TATGTATGTTTTCGAAG
>G362 Amino Acid Sequence (domain in AA coordinates: 62-82)
MSINPTMSRTGESSSGSSSDKTIKLFGFELISGSRTPEITTAESVSSSTNTTSLTVMKRH
ECQYCGKEFANSQALGGHQNAHKKERLKKKRLQLQARRASIGYYLTNHQQPITTSFQRQY
KTPSYCAFSSMHVNNDQMGVYNEDWSSRSSQINFGNNDTCQDLNEQSGEMGKLYGVRPNM
IQFQRDLSSRSDQMRSINSLDLHLGFAGDAA*
>G364 (64..516)
AAGCTTGATATCGCCTCTCTCTAATCTCTCTTTCTCTCTCTATCTCTAAGAATATATAAA
GGTATGGACTACCAGCCAAACACATCCCTACGTCTAAGCCTACCAAGTTACAAGAACCAC
CAACTAAACCTAGAACTTGTTCTCGAGCCTTCTTCCATGTCTTCTTCTTCATCTTCTTCC
ACGAACTCATCATCATGTTTGGAGCAGCCTAGGGTATTCTCATGTAACTATTGTCAAAGA
AAGTTTTACAGCTCTCAAGCTCTTGGTGGTCATCAAAACGCTCATAAGCTTGAGAGAACC
TTAGCCAAGAAGAGTCGAGAACTCTTTAGATCCTCAAACACTGTTGATTCTGATCAGCCT

TACCCGTTCTCCGGTCGCTTTGAGCTTTACGGCCGTGGCTACCAAGGATTTCTCGAAAGT
GGCGGCTCGAGGGACTTCTCCGCCCGCCGTGTGCCGGAGAGTGGTCTTGATCAGGATCAG
GAGAAGAGTCACCTTGACTTATCCTTAAGGCTCTAAAAGAATCTTATATTTTGTTAGTCT
ATATATTATCATATCAATTGTTAATCTTAAAATTGATTGTTTTACTTATTAGTCATTTCC
TATTATCTGAAAGTTTTCTTTGTAAGTTGTAACTATGGTCCTAAATTCAAATCCAAATTT
GATTTTGGAAGATGGTACCTAATGCAGTAGTTAAATAAGTTAAAAAAATGAAGGATCTAT
AATTCTCT
>G364 Amino Acid Sequence (domain in AA coordinates: 54-76)
MDYQPNTSLRLSLPSYKNHQLNLELVLEPSSMSSSSSSSTNSSSCLEQPRVFSCNYCQRK
FYSSQALGGHQNAHKLERTLAKKSRELFRSSNTVDSDQPYPFSGRFELYGRGYQGFLESG
GSRDFSARRVPESGLDQDQEKSHLDLSLRL*
>G365 (69..755)
CAATTCTTTTACTTTCATTCTCTTTATATATTCTCTCTACGCTATAATATATATTACACA
GAATATACATGGAACCGTCCATCAAAGGAGATCAAGAAATGTTAAAAATCAAGAAACAAG
GTCATCAAGATCTTGAGTTGGGGTTGACCCTTTTGTCACGTGGAACCGCGACCTCATCAG
AGCTCAATCTCATCGATTCTTTCAAAACCAGCTCATCATCGACTTCTCATCATCAGCACC
AGCAAGAACAATTGGCAGATCCGAGAGTGTTCTCGTGTAATTATTGTCAAAGAAAGTTCT
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GCCACGGTTCAGTCAGCAGATTCGCAAGCATGGCATCGTTACCATTACATGGCTCGGTGA
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GAAGACAAACGACGAGTTTAAGTCATGTTTTCAAACAGAGCATTCACCAGAAACCGACCA
TAGGAAAGATGTTGCCGGAGAAATTTCACCTTGAAGTCGCCGGAAATAATAACAGTAACA
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CATTATAACTTTTTTTATTCTCATCTTTGTTTGATATAATGATTGACGGCAGGGTGTGTT
AGAGTTTCACTAATGATCAAGTTGTACTTTTTATATATTTCATTGATACCTTGTTGATGT
AATTCAATATTTTAGGTCTGTTTTT
>G365 Amino Acid Sequence (domain in aa coordinates: 70-90)
MEPSIKGDQEMLKIKKQGHQDLELGLTLLSRGTATSSELNLIDSFKTSSSSTSHHQHQQE
QLADPRVFSCNYCQRKFYSSQALGGHQNAHKRERTLAKRGQYYKMTLSSLPSSAFAFGHG
SVSRFASMASLPLHGSVNNRSTLGIQAHSTIHKPSFLGRQTTSLSHVFKQSIHQKPTIGK
MLPEKFHLEVAGNNNSNMVAAKLERIGHFKSNQEDHNQFKKIDLTLKL*
>G367 (1..708)
ATGGACGCTTCAATAGTTTCCTCATCCACTGCTTTTCCATATCAAGATTCTCTAAACCAG
AGCATCGAAGACGAAGAAAGAGACGTTCATAATTCTAGTCACGAACTCAATCTCATCGAC
TGCATAGACGACACAACGAGTATCGTTAACGAATCTACAACATCCACAGAACAAAAGCTT
TTCTCATGCAACTATTGTCAAAGAACTTTCTATAGCTCACAAGCACTTGGTGGTCACCAA
AACGCACACAAGAGAGAGAGAGAACGTTGGCGAAGAGAGGACAACGTATGGCAGCGTCAGCC
TCAGCTTTTGGACATCCTTACGGTTTCTCTCCACTTCCTTTCCACGGACAGTACAACAAC
CATAGGTCTTTAGGGATCCAAGCGCATTCGATAAGCCACAAGCTAAGTTCTTATAACGGG
TTTGGTGGTCACTATGGTCAGATCAACTGGTCAAGACTTCCATTTGATCAACAACCAGCC
ATAGGTAAATTTCCCTCAATGGATAATTTTCATCATCATCATCATCAGATGATGATGATG
GCTCCTTCAGTAAATTCACGGTCCAATAACATCGATAGCCCAAGCAACACAGGACGGGTT
CTAGAAGGGTCACCGACTCTTGAACAATGGCACGGAGACAAAGGATTGTTGTTAAGTACA
AGTCATCATGAAGAGCAGCAGAAACTTGACTTGTCCCTCAAGCTTTGA
>G367 Amino Acid Sequence (domain in AA coordinates:63-84)
MDASIVSSSTAFPYQDSLNQSIEDEERDVHNSSHELNLIDCIDDTTSIVNESTTSTEQKL
FSCNYCQRTFYSSQALGGHQNAHKRERTLAKRGQRMAASASAFGHPYGFSPLPFHGQYNN
HRSLGIQAHSISHKLSSYNGFGGHYGQINWSRLPFDQQPAIGKFPSMDNFHHHHHQMMMM
APSVNSRSNNIDSPSNTGRVLEGSPTLEQWHGDKGLLLSTSHHEEQQKLDLSLKL*
>G373 (1..1854)
ATGGCGATTGAAACTCAGCTTCCTTGCGACGGTGACGGTGTGTGTATGCGGTGTCAGGTG
AATCCTCCGTCAGAAGAGACTCTCACTTGTGGCACGTGCGTCACTCCATGGCACGTGCCG
TGTCTCCTCCCCGAATCACTCGCTTCTTCCACTGGAGAGTGGGAGTGTCCCGATTGCTCC
GGCGTTGTCGTTCCCTCCGCCGCTCCGGGTACCGGAAACGCTCGACCTGAATCTTCCGGT
TCAGTTCTCGTTGCTGCGATCCGTGCGATTCAGGCTGATGAGACTTTAACCGAAGCTGAG

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GAGAAGAAGAAGTTAGAAATCTTTTGTTCTATTTGCATTCAATTGCCAGAAAGACCTATC
ACGACACCGTGTGGGCACAATTTCTGTTTGAAATGTTTCGAGAAATGGGCAGTAGGTCAA
GGGAAGCTAACTTGTATGATATGCCGAAGCAAAATTCCGAGACATGTGGCAAAAAATCCT
CGCATCAACTTAGCTCTAGTTTCTGCTATTCGTTTAGCAAATGTTACCAAATGTTCTGTT
GAGGCAACTGCAGCCAAGGTTCATCATATTATCCGCAACCAAGACCGTCCTGAGAAAGCA
TTTACTACCGAGCGGGCAGTAAAAACTGGGAAAGCTAATGCTGCTAGCGGTAAGTTTTTT
GTGACAATACCTCGTGATCATTTTGGTCCCATACCAGCTGAGAATGATGTCACTAGAAAG
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CATTTCCCGCATATTGCTGGCATTGCCGGGCAATCAGCGGTTGGAGCTCAGTCTGTGGCC
CTCTCTGGAGGTTATGACGATGATGAGGATCATGGTGAATGGTTTCTCTACACAGGAAGT
GGTGGAAGGGATCTCAGTGGAAACAAAAGAATTAACAAGAAACAGTCGTCTGACCAGGCG
TTTAAAAACATGAATGAATCTCTAAGACTTAGTTGCAAAATGGGCTATCCTGTCCGAGTT
GTCAGGTCTTGGAAGGAGAAGCGTTCTGCATATGCCCCTGCTGAAGGTGTGAGATATGAT
GGGGTCTATCGAATTGAGAAGTGCTGGAGTAATGTTGGAGTACAGGGTTCTTTTAAGGTC
TGTCGTTACCTGTTTGTTAGATGTGACAATGAGCCAGCTCCATGGACCAGTGATGAGCAT
GGCGATCGTCCAAGACCGTTGCCTAATGTTCCGGAGCTTGAGACTGCTGCTGACCTGTTT
GTGAGAAAGGAGAGTCCATCATGGGATTTCGATGAAGCTGAGGGTCGTTGGAAATGGATG
AAGTCTCCTCCTGTTAGCAGAATGGCTTTGGATCCTGAGGAGAGGAAGAAGAATAAGAGA
GCAAAAAATACTATGAAGGCCAGACTTCTGAAAGAATTTAGTTGCCAAATCTGTCGGGAA
GTGCTGAGTCTTCCAGTGACGACGCCTTGTGCACACAACTTCTGCAAAGCATGCTTAGAA
GCGAAGTTTGCTGGGATAACTCAACTGAGAGAGAGAAGCAATGGCGGACGTAAACTACGT
GCAAAGAAGAACATCATGACCTGCCCTTGCTGCACGACGGATCTCTCCGAGTTTCTCCAA
AACCCGCAGGTGAACAGAGAGATGATGGAGATAATAGAGAATTTTAAGAAGAGTGAGGAA
GAGGCTGATGCATCCATTTCTGAAGAAGAAGAAGAAGAATCCGAACCTCCAACTAAGAAG
ATTAAGATGGATAACAACTCTGTTGGTGGTAGTGGTACAAGTCTCTCAGCTTAA
>G373 Amino Acid Sequence (domain in AA coordinates: 129-168)
MAIETQLPCDGDGVCMRCQVNPPSEETLTCGTCVTPWHVPCLLPESLASSTGEWECPDCS
GVVVPSAAPGTGNARPESSGSVLVAAIRAIQADETLTEAEKAKKRQKLMSGGGDDGVDEE
EKKKLEIFCSICIQLPERPITTPCGHNFCLKCFEKWAVGQGKLTCMICRSKIPRHVAKNP
RINLALVSAIRLANVTKCSVEATAAKVHHIIRNQDRPEKAFTTERAVKTGKANAASGKFF
VTIPRDHFGPIPAENDVTRKQGVLVGESWEDRQECRQWGAHFPHIAGIAGQSAVGAQSVA
LSGGYDDDEDHGEWFLYTGSGGRDLSGNKRINKKQSSDQAFKNMNESLRLSCKMGYPVRV
VRSWKEKRSAYAPAEGVRYDGVYRIEKCWSNVGVQGSFKVCRYLFVRCDNEPAPWTSDEH
GDRPRPLPNVPELETAADLFVRKESPSWDFDEAEGRWKWMKSPPVSRMALDPEERKKNKR
AKNTMKARLLKEFSCQICREVLSLPVTTPCAHNFCKACLEAKFAGITQLRERSNGGRKLR
AKKNIMTCPCCTTDLSEFLQNPQVNREMMEIIENFKKSEEEADASISEEEEEESEPPTKK
IKMDNNSVGGSGTSLSA*
>G396 (1..957)
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GAACCATCTCTGAGGTTGAATCTTATGCCGTTGACAACTTCTTCTTCTTCTTCTTCGTTT
CAACACATGCACAATCAGAATAACAATAGCCATCCCCAGAAGATTCATAACATCTCTTGG
ACTCATCTGTTTCAATCTTCTGGGATTAAACGTACAACTGCAGAGAGAAACTCCGACGCC
GGGTCATTTCTAAGAGGTTTCAACGTGAACAGAGCTCAGTCTTCGGTGGCGGTAGTGGAC
TTGGAAGAAGAAGCCGCCGTCGTCTCGTCTCCAAACAGCGCCGTTTCGAGTCTGAGTGGA
AATAAAAGGGATCTTGCGGTGGCGAGAGGAGGAGATGAAAACGAGGCGGAGAGAGCTTCT
TGCTCACGCGGAGGGGGAAGCGGTGGTAGCGACGATGAAGACGGCGGAAACGGCGACGGA
TCAAGGAAGAAACTACGGTTATCGAAGGATCAAGCTCTTGTTCTCGAGGAGACTTTTAAA
GAACATAGCACTCTTAATCCGAAGCAAAAGCTGGCTCTAGCAAAACAGTTGAATCTAAGG
GCAAGACAAGTTGAAGTGTGGTTTCAGAACCGTAGGGCAAGGACGAAGCTGAAACAAACG
GAGGTTGATTGTGAGTATTTAAAGAGATGTTGCGATAATCTGACCGAGGAGAATCGACGG
CTGCAGAAAGAAGTGTCGGAGCTGAGGGCGTTGAAGTTGTCTCCACATCTCTACATGCAC
ATGACTCCTCCTACTACTCTCACCATGTGCCCTTCTTGCGAACGTGTCTCCTCCTCTGCC
GCCACTGTGACCGCTGCTCCTTCCACTACTACTACTCCTACGGTGGTGGGGCGGCCAAGT
CCACAGCGATTAACTCCTTGGACTGCTATTTCTCTCCAGCAAAAATCAGGTCGCTAG
>G396 Amino Acid Sequence (domain in AA coordinates: 159-220)
MGERDDGLGLSLSLGNSQQKEPSLRLNLMPLTTSSSSSFQHMHNQNNNSHPQKIHNISW

THLFQSSGIKRTTAERNSDAGSFLRGFNVNRAQSSVAVVDLEEEAAVVSSPNSAVSSLSG
NKRDLAVARGGDENEAERASCSRGGGSGGSDDEDGGNGDGSRKKLRLSKDQALVLEETFK
EHSTLNPKQKLALAKQLNLRARQVEVWFQNRRARTKLKQTEVDCEYLKRCCDNLTEENRR
LQKEVSELRALKLSPHLYMHMTPPTTLTMCPSCERVSSSAATVTAAPSTTTTPTVVGRPS
PQRLTPWTAISLQQKSGR*
>G431 (1..1149)
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GGTCCGATGTGTCCTATGATGATGATGATGCCGCCCATCATGACATCACATCAACATCAT
GGTCATGATCATCAACATCAACAACAAGAACATGATGGTTATGCATATCAGTCACACCAC
CAACAAAGTAGTTCCCTTTTTCTTCAATCACTAGCTCCTCCCCAAGGAACTAAGAACAAA
GTTGCTTCTTCTTCTTCTCCTTCCTCTTGTGCTCCTGCCTATTCTCTAATGGAGATCCAT
CATAACGAAATCGTTGCAGGAGGAATCAACCCTTGCTCCTCTTTCTCTTCTTCAGCCTCT
GTCAAGGCCAAGATCATGGCTCATCCTCACTACCACCGCCTCTTGGCCGCTTATGTCAAT
TGTCAGAAGGTTGGAGCACCACCGGAGGTTGTGGCGAGGCTGGAGGAGGCATGCTCGTCT
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CCTTTCAAGGAAGCTATGGTCTTCCTTCAACGTGTCGAGTGTCAATTCAAATCCCTCTCT
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AGAGAGCTTAAAGGACAGCTCTTGCGCAAGTACAGTGGTTACTTAGGGAGCCTCAAGCAA
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GATTGGTGGAGCCGTCACTACAAATGGCCTTACCCTTCGGAGCAACAAAAGCTCGCCCTT
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ATGCTTTGA
>G431 Amino Acid Sequence (domain in AA coordinates: 286-335)
MESGSNSTSCPMAFAGDNSDGPMCPMMMMMPPIMTSHQHHGHDHQHQQQEHDGYAYQSHH
QQSSSLFLQSLAPPQGTKNKVASSSSPSSCAPAYSLMEIHHNEIVAGGINPCSSFSSSAS
VKAKIMAHPHYHRLLAAYVNCQKVGAPPEVVARLEEACSSAAAAAASMGPTGCLGEDPGL
DQFMEAYCEMLVKYEQELSKPFKEAMVFLQRVECQFKSLSLSSPSSFSGYGETAIDRNNN
GSSEEEVDMNNEFVDPQAEDRELKGQLLRKYSGYLGSLKQEFMKKRKKGKLPKEARQQLL
DWWSRHYKWPYPSEQQKLALAESTGLDQKQINNWFINQRKRHWKPSEDMQFVVMDATHPH
HYFMDNVLDNPFPMDHISSTML*
>G479 (1..1128)
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TCCTCCACTGAGTCATCCTCTTTCAGTGGAGGGCTCATGTTTGGCCAGAAGATCTACTTC
GAGGACGGTGGTGGTGGATCCGGGTCTTCTTCCTCAGGTGGTCGTTCAAACAGACGTGTC
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>G479 Amino Acid Sequence (conserved domain in AA coordinates:70-149)
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FHQLPEFDLEKRSCRRRLAGHNERRRKPQPASLSVLASRYGRIAPSLYENGDAGMNGSFL
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>G546 (1..588)
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>G546 Amino Acid Sequence (domain in AA coordinates:114-155)
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>G551 (1..708)
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>G551 Amino Acid Sequence (conserved domain in AA coordinates:73-133)
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>G578 (1..978)
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>G578 Amino Acid Sequence (domain in AA coordinates 36-96)
MHSLNETVIPDVDYMQSDRGHMHAAASDSSDRSKDKLDQKTLRRLAQNREAARKSRLRKK
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CFLWLGGFPSSELLKLLANQLEPMTERQVMGINSLQQTSQQAEDALSQGMESLQQSLADT
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ALLAIHDYSSRLRALSSLWLARPRE*
>G596 (168..1121)
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>G596 Amino Acid Sequence (domain in AA coordinates: 89-96)
MDQVSRSLPPPFLSRDLHLHPHHQFQHQQQQQQNHGHDIDQHRIGGLKRDRDADIDPNE
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SVQLPAEAYWGTPRPSF*
>G617 (59..1141)
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>G617 Amino Acid Sequence (domain in AA coordinates: 64-118)
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>G620 (40..666)
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>G620 Amino Acid Sequence (domain in AA coordinates: 20-118)
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>G625 (151..1137)
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>G625 Amino Acid Sequence (conserved domain in AA coordinates:52-119)
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>G658 (17..757)
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>G658 Amino Acid Sequence (domain in AA coordinates: 2-105)
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SDVRTH*
>G716 (271..2079)
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>G716 Amino Acid Sequence (domain in AA coordinates: 24-355)
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>G725 (46..1122)
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CAAGTGCTATGTGAACATCCAAATCTGGAATGATGAATCAGCACTAGGTCTTCTCTTTGA
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>G920 Amino Acid Sequence (domain in AA coordinates: 152-211)
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>G939 (9..1565)
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>G939 Amino Acid Sequence (domain in AA coordinates: 97-106)
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>G963 (1..897)
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TGGTACTTTTACAGCACAAGGGATAAGAAGTATCCAAATGGCTCTAGGACGAACCGTGCG
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>G963 Amino Acid Sequence (domain in AA coordinates: TBD)
MSLPPGFRFHPTDEELVAYYLDRKVNGQAIELEIIPEVDLYKCEPWDLPEKSFLPGNDME
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TNWVMHEYRLTHAPSSSLKESYALCRVFKKNIQIPKRKGEEEEAEEESTSVGKEEEEEKE
KKWRKCDGNYIEDESLKRASAETSSSELTQGVLLDEANSSSIFALHFSSSLLDDHDHLFS
NYSHQLPYHPPLQLQDFPQLSMNEAEIMSIQQDFQCRDSMNGTLDEIFSSSATFPASL*
>G979 (60..1352)
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>G979 Amino Acid Sequence (domain in AA coordinates: 63-139,165-233)
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TTSVSCNYLV*
>G987 (1..4011)
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>G987 Amino Acid Sequence (domain in AA coordinates: 428-432,704-708)
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HCAQAISTGDKTTALEFLLQIRQQSSPLGDAGQRLAHCFANALEARLQGSTGPMIQTYYN
ALTSSLKDTAADTIRAYRVYLSSSPFVTLMYFFSIWMILDVAKDAPVLHIVDFGILYGFQ
WPMFIQSISDRKDVPRKLRITGIELPQCGFRPAERIEETGRRLAEYCKRFNVPFEYKAIA
SQNWETIRIEDLDIRPNEVLAVNAGLRLKNLQDETGSEENCPRDAVLKLIRNMNPDVFIH
AIVNGSFNAPFFISRFKEAVYHYSALFDMFDSTLPRDNKERIRFEREFYGREAMNVIACE
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GWKGRTLYASSCWVPA*

>G993 (6..1091)

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>G993 Amino Acid Sequence (domain in AA coordinates: 69-134)

MEYSCVDDSSTTSESLSISTTPKPTTTTEKKLSSPPATSMRLYRMGSGGSSVVLDSENGV
ETESRKLPSSKYKGVVPQPNGRWGAQIYEKHQRVWLGTFNEEEEAASSYDIAVRRFRGRD
AVTNFKSQVDGNDAESAFLDAHSKAEIVDMLRKHTYADEFEQSRRKFVNGDGKRSGLETA
TYGNDAVLRAREVLFEKTVTPSDVGKLNRLVIPKQHAEKHFPLPAMTTAMGMNPSPTKGV
LINLEDRTGKVWRFRYSYWNSSQSYVLTKGWSRFVKEKNLRAGDVVCFERSTGPDRQLYI
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L*

>G681 (1..804)

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>G681 Amino Acid Sequence (domain in AA coordinates:14-120)

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IDPMTHEPIIKHLTVNTTNADCGNSSTTTSPSTTESSPSSGSSRLLNKLAAGISSRQHSL
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IDAMDMYEMTSYDAVMYESSHILDHLF*
>G1482 (1..996)
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AAACATCTCCGTTTCTCTCTCCTTTATCCTTCTTCTTCCAACACCTCCTCTCCTCTCTGC
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>G1482 Amino Acid Sequence (domain in aa coordinates: 5-63)
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>G225 (157..441)
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>G225 Amino Acid Sequence (domain in AA coordinates: 39-76)
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>G226 (10..348)
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>G226 Amino Acid Sequence (domain in AA coordinates: 28-78)
MDNTNRLRLRRGPSLRQTKFTRSRYDSEEVSSIEWEFISMTEQEEDLISRMYRLVGNRWD
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>G9 (81..1139)
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>G9 Amino Acid Sequence (domain in AA coordinates: 62-127)
MDSSCIDEISSSTSESFSATTAKKLSPPPAAALRLYRMGSGGSSVVLDPENGLETESRKL
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>G1040 (51..863)
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>G1040 Amino Acid Sequence (domain in AA coordinates: 109-158)
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>G2114 (64..1311)
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>G2114 Amino Acid Sequence (conserved domain in AA coordinates:221-297, 323-393)
MKKWLGFSLTPPLRICNSEEEELRHDGSDVWRYDINFDHHHHDEDVPKVEDLLSNSHQTE
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>G450 (65..751)
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>G450 Amino Acid Sequence (domain in AA coordinates: TBD)
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>G584 (40..1809)
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>G584 Amino Acid Sequence (domain in AA coordinates: 401-494)
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>G668 (1..1056)
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>G668 Amino Acid Sequence (domain in AA coordinates: 13-113)
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>G1050 (23..1582)
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>G1050 Amino Acid Sequence (domain in AA coordinates: 372-425)
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>G1463 (199..1209)
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>G1463 Amino Acid Sequence (conserved domain in AA coordinates:9-156)
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>G1944 (236..1306)
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>G2383 (37..990)

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>G2383 Amino Acid Sequence (conserved domain in AA coordinates:89-149)
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>G571 (326..1708)
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>G571 Amino Acid Sequence (domain in AA cordinates: 160-220)
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>G636 (6..1814)
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>G1134 (61..849)
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>G1020 Amino Acid Sequence (domain in AA coordinates:28-95)
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>G1023 Amino Acid Sequence (conserved domain in AA coordinates:128-195)
MAERKKRSSIQTNKPNKKPMKKKPFQLNHLPGLSEDLKTMRKLRFVVNDPYATDYSSSEE
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>G1053 (38..538)
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>G1053 Amino Acid Sequence (domain in AA coordinates: 74-120)
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>G1137 (202..1248)
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>G1137 Amino Acid Sequence (domain in AA coordinates:264-314)
MPLDKRQRDLPLGLSPQACFKDIVGRSVLPRIPLPELGKLYAAKLQARCLQPPPFQSLLC
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FPSHAAAEPVKLSELQGIEKAFKEDGEEFHKSDGTESEMHEDTEEINALLYSDDDYDDDC
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>G1181 (113..1012)
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>G1181 Amino Acid Sequence (domain in AA coordinates: 24-114)
MNSPPVDAMITGESSSQRSIPTPFLTKTFNLVEDSSIDDVISWNEDGSSFIVWNPTDFAK
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>G1228 (63..1139)
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>G1228 Amino Acid Sequence (domain in AA coordinates: 179-233)
MERFQGHINPCFFDRKPDVRSLEVQGFAEAQSFAFKEKEEESLQDTVPFLQMLQSEDPSS
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IAVERNRRRQMNEHINSLRALLPPSYIQRGDQASIVGGAINYVKVLEQIIQSLESQKRTQ
QQSNSEVVENALNHLSGISSNDLWTTLEDQTCIPKIEATVIQNHVSLKVQCEKKQGQLLK
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>G1277 (51..512)
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TCAGAATGAGAAAATGGGGGAAATGGGTTGCGGAGATTCGAGAACCCAACAAGCGTTCAA
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>G1277 Amino Acid Sequence (domain in AA coordinates: 18-85)
MDAGVAVKADVAVKMKRERPFKGIRMRKWGKWVAEIREPNKRSRLWLGSYSTPEAAARAY
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FSQKRDFGGGLLELVDLNKLPDPENLDDDLVGK*
>G1309 (53..859)
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>G1309 Amino Acid Sequence (domain in AA coordinates: 9-114)
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>G1314 (1..990)
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>G1314 Amino Acid Sequence (domain in AA coordinates: 14-116)
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>G1317 (1..849)
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ATGTTTTAA

>G1317 Amino Acid Sequence (conserved domain in AA coordinates:13-118)
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>G1323 (49..870)
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>G1323 Amino Acid Sequence (domain in AA coordinates: 15-116)
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>G1332 (1..606)
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>G1332 Amino Acid Sequence (conserved domain in AA coordinates:13-116)
MECKREEGKSYVKRGLWKPEEDMILKSYVETHGEGNWADISRRSGLKRGGKSCRLRWKNY
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>G1334 (76..885)
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MQTEELLSPPQTPWWNAFGSQPLTTESLSGEASDSFTGVKAVTTEAEQGVVDKQTSTTLF
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RVMIPLKMETEEDGTIYVNSKQYHGIIRRRQSRAKAEKLSRCRKPYMHHSRHLHAMRRPR
GSGGRFLNTKTADAAKQSKPSNSQSSEVFHPENETINSSREANESNLSDSAVTSMDYFLS
SSAYSPGGMVMPIKWNAAAMDIGCCKLNI*
>G1381 (32..802)
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TGACTCCGGAGGGAAACGGCGGAAGAGCAACGTTAGTGATGATAACAAGAATCCGACGTC
GTATAGAGGAGTGAGGATGAGGAGTTGGGGAAAATGGGTGTCGGAGATTAGAGAGCCGAG
GAAGAAATCAAGAATATGGCTTGGCACTTATCCAACGGCAGAGATGGCAGCTCGTGCTCA
TGATGTGGCGGCTTTAGCTATTAAAGGCAACTCCGGTTTTCTTAATTTCCCTGAATTATC
CGGTTTGCTTCCTCGTCCGGTTAGCTGCTCTCCTAAGGATATACAAGCTGCAGCTACCAA
AGCCGCCGAAGCAACCACGTGGCACAAACCGGTTATCGATAAGAAATTAGCTGATGAGCT
AAGCCACTCTGAGTTGTTGTCTACCGCTCAGTCTTCGACTTCTAGTAGTTTCGTGTTTTC
TTCGGACACGTCGGAGACTTCTAGTACGGACAAGGAAAGCAACGAAGAGACGGTGTTTGA
TTTGCCGGACCTTTTCACGGACGGGCTTATGAACCCAAACGATGCGTTTTGTTTATGCAA
CGGCACCTTTACGTGGCAGCTTTACGGAGAGGAGGATGTAGGGTTCAGGTTTGAAGAGCC
GTTTAATTGGCAAAATGACTAAACCGCCCTCCACTTGCTTACTGTAATTACTAACATATA
ATTTTCTTGATAAAGAACATATATTTCCATTACGGTATTAACTAATCTTTTCTATCCTTT
TCTCTTTTCTTGTTTCTACATCTGAGTATATTGTCACTATGTGAAAAAATTGATCTCGTT
TTGAATATTTACTTTTCAAAATTGAAGTAACGCAAGTGATTGATAAAAAAAAAAAAA
>G1381 Amino Acid Sequence (domain in AA coordinates: TBD)
MGKQINIESSATHHQDNIVSVITATISSSSVVTSSSDSWSTSKRSLVQDNDSGGKRRKSN
VSDDNKNPTSYRGVRMRSWGKWVSEIREPRKKSRIWLGTYPTAEMAARAHDVAALAIKGN
SGFLNFPELSGLLPRPVSCSPKDIQAAATKAAEATTWHKPVIDKKLADELSHSELLSTAQ
SSTSSSFVFSSDTSETSSTDKESNEETVFDLPDLFTDGLMNPNDAFCLCNGTFTWQLYGE
EDVGFRFEEPFNWQND*
>G1382 (90..1763)
CTCTCATTTCGCCATAGCTGAGAGCTTCTTCTACTTTCCCTTAGCTTCTTTTTTCCTTCA
TTTTTGTTCTACCCTTGCGAATCTCTGAAATGAACCCTCAAGCTAATGACCGGAAGGAGT
TTCAGGGAGATTGTTCGGCGACGGGAGATCTCACGGCAAAGCACGATTCAGCTGGAGGAA
ACGGAGGTGGAGGTGCTAGGTATAAGCTGATGTCACCGGCCAAGCTTCCGATCTCGAGGT
CGACTGATATCACGATTCCTCCTGGGTTGAGTCCGACTTCGTTTTTGGAATCTCCTGTTT
TCATCTCCAACATCAAGCCAGAACCTTCCCCTACTACTGGTTCTTTGTTCAAGCCTCGAC
CAGTGCACATTTCTGCTAGCTCAAGTTCTTATACAGGCAGGGGGTTCCATCAGAACACCT
TTACTGAGCAGAAGTCCAGTGAATTTGAGTTCAGACCTCCTGCATCAAATATGGTATATG
CAGAGCTTGGCAAGATTAGAAGTGAGCCACCAGTACATTTTCAAGGCCAGGGCCATGGAT
CCTCACACTCACCTTCTTCGATCAGTGATGCTGCAGGTTCCTCAAGTGAGCTAAGCCGGC
CAACTCCTCCTTGTCAGATGACACCAACGAGCTCAGATATTCCGGCTGGATCTGATCAAG

AGGAATCAATCCAGACTTCCCAAAATGACTCCAGAGGAAGCACTCCATCCATCTTGGCTG
ATGATGGTTATAACTGGAGAAAATATGGTCAAAAGCATGTCAAAGGGAGTGAATTTCCCC
GGAGCTATTATAAATGTACACATCCTAATTGTGAAGTGAAAAAGTTATTTGAAAGATCTC
ATGATGGGCAGATCACCGATATTATATACAAGGGTACACATGACCATCCTAAACCTCAAC
CTGGTCGCCGAAACTCTGGTGGTATGGCTGCACAAGAAGAAAGGCTAGACAAGTATCCTT
CTTCAACTGGCCGAGATGAGAAGGGATCTGGCGTCTACAACTTGTCTAACCCCAATGAAC
AAACTGGTAACCCTGAAGTACCTCCTATCTCAGCATCTGACGATGGTGGAGAAGCGGCAG
CGTCAAATAGGAATAAAGATGAGCCGGACGATGATGATCCATTCTCAAAACGGAGGAGGA
TGGAGGGTGCGATGGAAATAACTCCACTAGTGAAACCCATCCGGGAGCCTCGGGTTGTTG
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AGAAAGTCGTAAGGGGGAACCCAAATCCCAGGAGCTACTACAAATGCACAGCTCATGGAT
GCCCAGTGAGAAAACACGTGGAGAGAGCATCACATGATCCAAAAGCTGTAATAACAACAT
ACGAAGGCAAACACGATCATGATGTTCCCACTTCAAAGTCTAGCAGCAATCACGAAATCC
AGCCTCGGTTCAGACCAGATGAAACAGACACCATCAGCCTCAATCTTGGTGTTGGAATCT
CATCTGATGGACCTAACCACGCTTCCAACGAACATCAGCACCAGAATCAACAACTTGTCA
ACCAAACTCACCCAAATGGAGTCAATTTCAGGTTTGTTCATGCTAGTCCCATGTCATCCT
ACTATGCTAGCTTAAATAGCGGTATGAATCAGTACGGCCAGAGAGAAACAAAGAACGAGA
CTCAAAATGGTGACATCTCGTCCTTGAACAATTCATCTTACCCATATCCGCCCAACATGG
GGAGAGTACAATCGGGTCCGTAAAACAAAAAGTAAGCAACATTATGTACGGGATCTTCTT
AGGTTAGGAATGGGACGAGGCCTTGTTCTATATAATTCCTATTTCTTCACAGAGAGCTGA
TCTTGATTCAAACTATCTCCACCATATATATTTGTTTGTGTCACCTGTATTGAGTTCCAA
AAATGTTATGTAAAAATACACAACAAGATGTTAATGCTTTTATTTAAACAAGAAACAGCA
ATATTACTACAAAAAAAAAAAAAAAAAAA

>G1382 Amino Acid Sequence (domain in AA coordinates: 210-266, 385-437)
MNPQANDRKEFQGDCSATGDLTAKHDSAGGNGGGGARYKLMSPAKLPISRSTDITIPPGL
SPTSFLESPVFISNIKPEPSPTTGSLFKPRPVHISASSSSYTGRGFHQNTFTEQKSSEFE
FRPPASNMVYAELGKIRSEPPVHFQGQGHGSSHSPSSISDAAGSSSELSRPTPPCQMTPT
SSDIPAGSDQEESIQTSQNDSRGSTPSILADDGYNWRKYGQKHVKGSEFPRSYYKCTHPN
CEVKKLFERSHDGQITDIIYKGTHDHPKPQPGRRNSGGMAAQEERLDKYPSSTGRDEKGS
GVYNLSNPNEQTGNPEVPPISASDDGGEAAASNRNKDEPDDDDPFSKRRRMEGAMEITPL
VKPIREPRVVVQTLSEVDILDDGYRWRKYGQKVVRGNPNPRSYYKCTAHGCPVRKHVERA
SHDPKAVITTYEGKHDHDVPTSKSSSNHEIQPRFRPDETDTISLNLGVGISSDGPNHASN
EHQHQNQQLVNQTHPNGVNFRFVHASPMSSYYASLNSGMNQYGQRETKNETQNGDISSLN
NSSYPYPPNMGRVQSGP*

>G1435 (8..904)
GTGAAACATGGGGAAGGAAGTTATGGTGAGCGATTACGGTGACGACGACGGAGAAGACGC
CGGCGGCGGCGATGAATATAGGATTCCGGAATGGGAAATTGGTTTACCCAACGGAGATGA
TTTGACTCCGTTATCTCAATATCTAGTCCCGTCGATTCTCGCGTTAGCTTTCAGCATGAT
CCCAGAACGAAGCCGTACAATTCACGACGTCAATCGCGCGTCGCAAATCACGCTCTCTTC
GTTGAGAAGCAGTACCAATGCTTCGTCTGTGATGGAGGAGGTCGTGGATCGAGTTGAATC
GAGTGTTCCAGGATCAGATCCGAAGAAACAGAAGAAATCGGATGGTGGTGAAGCAGCGGC
GGTGGAGGATTCCACGGCGGAGGAAGGAGACTCCGGGCCTGAAGACGCGTCTGGGAAGAC
ATCGAAACGACCGCGTTTAGTGTGGACACCGCAGCTACACAAGAGATTTGTGGACGTTGT
GGCTCATCTAGGGATTAAAAACGCAGTGCCGAAGACGATTATGCAGCTGATGAACGTGGA
AGGACTTACTCGTGAGAACGTTGCGTCTCATTTGCAGAAATATAGGCTTTACCTTAAACG
GATTCAAGGATTGACGACGGAAGAAGATCCTTATTCGTCGTCGGATCAGCTCTTCTCTTC
AACGCCGGTTCCTCCACAGAGCTTTCAAGACGGCGGAGGAAGTAACGGAAAGTTGGGGGT
TCCGGTTCCGGTTCGGTCGATGGTGCCTATTCCAGGCTATGGGAATCAAATGGGTATGCA
AGGATATTATCAACAGTATAGTAACCATGGCAATGAATCAAACCAATATATGATGCAGCA
GAATAAGTTTGGAACAATGGTGACATATCCTTCTGTTGGTGGTGGTGACGTGAATGACAA
GTAAATGGATCTTAAAGGTCTATAATTTGCTCTACAGAGAGATACTGGTTCTTGGCTTAT
GGTTTATTTTCCCACTTCATGAGGTTGTTGTGACTTTTAATTCTCCATGTTTTCCACACA
AGTCTTTATTGCCTTTGTATAGAAAATGATTTCGAGAAAATCACTGGGAAGCTTGGTATT
GTTGGAGGATGAAGCCTTCTATGAATGATTTAGTTTCCTACTGTCTCCATTCTTTATGAG
GTAATAAAGCCTTCTTTTGCTCATCGCTTGTAGTCTTCTTAAATTCAAGACAGCGTCACA
TGTTTGTTCGGTTATGTTAATTGTTTCTTTCTTTGGATAATGAAGATAGCATCAGGTCTC
ATGTCTCCTCACTTTGATAAA

>G1435 Amino Acid Sequence (domain in AA coordinates: 146-194)
MGKEVMVSDYGDDDGEDAGGGDEYRIPEWEIGLPNGDDLTPLSQYLVPSILALAFSMIPE
RSRTIHDVNRASQITLSSLRSSTNASSVMEEVVDRVESSVPGSDPKKQKKSDGGEAAAVE
DSTAEEGDSGPEDASGKTSKRPRLVWTPQLHKRFVDVVAHLGIKNAVPKTIMQLMNVEGL
TRENVASHLQKYRLYLKRIQGLTTEEDPYSSSDQLFSSTPVPPQSFQDGGGSNGKLGVPV
PVPSMVPIPGYGNQMGMQGYYQQYSNHGNESNQYMMQQNKFGTMVTYPSVGGGDVNDK*
>G1537 (1..783)
ATGGAAAACGAAGTAAACGCAGGAACAGCAAGCAGTTCAAGATGGAACCCAACGAAAGAT
CAGATCACGCTACTGGAAAATCTTTACAAGGAAGGAATACGAACTCCGAGCGCCGATCAG
ATTCAGCAGATCACCGGTAGGCTTCGTGCGTACGGCCATATCGAAGGTAAAAACGTCTTT
TACTGGTTCCAGAACCATAAGGCTAGGCAACGCCAAAAGCAGAAACAGGAGCGCATGGCT
TACTTCAATCGCCTCCTCCACAAAACCTCCCGTTTCTTCTACCCCCCTCCTTGCTCAAAC
GTGGGTTGTGTCAGTCCGTACTATTTACAGCAAGCAAGTGATCATCATATGAATCAACAT
GGAAGTGTATACACAAACGATCTTCTTCACAGAAACAATGTGATGATTCCAAGTGGTGGC
TACGAGAAACGGACAGTCACACAACATCAGAAACAACTTTCAGACATAAGAACAACAGCA
GCCACAAGAATGCCAATTTCTCCGAGTTCACTCAGATTTGACAGATTTGCCCTCCGTGAT
AACTGTTATGCCGGTGAGGACATTAACGTCAATTCCAGTGGACGGAAAACACTCCCTCTT
TTTCCTCTTCAGCCTTTGAATGCAAGTAATGCTGATGGTATGGGAAGTTCCAGTTTTGCC
CTTGGTAGTGATTCTCCGGTGGATTGTTCTAGCGATGGAGCCGGCCGAGAGCAGCCGTTT
ATTGATTTCTTTTCTGGTGGTTCTACTTCTACTCGTTTCGATAGTAATGGTAATGGGTTG
TAA
>G1537 Amino Acid Sequence (domain in AA coordinates: 14-74)
MENEVNAGTASSSRWNPTKDQITLLENLYKEGIRTPSADQIQQITGRLRAYGHIEGKNVF
YWFQNHKARQRQKQKQERMAYFNRLLHKTSRFFYPPPCSNVGCVSPYYLQQASDHHMNQH
GSVYTNDLLHRNNVMIPSGGYEKRTVTQHQKQLSDIRTTAATRMPISPSSLRFDRFALRD
NCYAGEDINVNSSGRKTLPLFPLQPLNASNADGMGSSSFALGSDSPVDCSSDGAGREQPF
IDFFSGGSTSTRFDSNGNGL*
>G1545 (67..729)
CATCACCAATCTTTTGAATCTAAGAGAGAGAAGAAGAAGAAGGTCTAGAGAACGAAAAGA
AGAAACATGAATAACCAGAATGTAGATGATCATAATCTTCTACTCATTTCTCAATTGTAC
CCTAATGTCTATACTCCATTAGTACCACAACAAGGAGGAGAAGCAAAACCAACACGGCGG
AGGAAAAGGAAGAGCAAGAGTGTTGTGGTGGCAGAGGAGGGTGAAAACGAAGGCAATGGG
TGGTTTAGAAAGAGAAAATTGAGTGATGAGCAAGTAAGAATGTTGGAGATTAGCTTTGAA
GACGATCATAAGCTTGAATCCGAGAGGAAAGATCGGCTTGCTTCTGAGTTAGGGCTTGAT
CCTCGTCAAGTCGCCGTCTGGTTCCAAAACCGCCGTGCACGGTGGAAGAACAAACGAGTC
GAGGATGAATACACTAAACTCAAGAATGCATACGAAACCACCGTCGTTGAGAAATGTCGT
CTTGATTCTGAGGTTATTCACCTAAAGGAACAACTTTACGAGGCTGAAAGAGAGATCCAA
CGGCTTGCAAAAAGAGTTGAAGGAACTTTAAGTAACAGTCCTATCTCATCCTCTGTGACC
ATTGAAGCCAATCATACGACACCGTTTTTTGGAGATTACGACATCGGATTTGACGGTGAG
GCTGACGAGAACTTGCTCTACTCGCCAGATTACATTGATGGATTAGACTGGATGAGCCAA
TTTATGTAAAAAACTATAAGCTAATCTATTTTCAGTCGTAGTATAG
>G1545 Amino Acid Sequence (domain in AA coordinates: 54-117)
MNNQNVDDHNLLLISQLYPNVYTPLVPQQGGEAKPTRRRKRKSKSVVVAEEGENEGNGWF
RKRKLSDEQVRMLEISFEDDHKLESERKDRLASELGLDPRQVAVWFQNRRARWKNKRVED
EYTKLKNAYETTVVEKCRLDSEVIHLKEQLYEAEREIQRLAKRVEGTLSNSPISSSVTIE
ANHTTPFFGDYDIGFDGEADENLLYSPDYIDGLDWMSQFM*
>G1641 (1..867)
ATGGAGGTTATGAGACCGTCGACGTCACACGTGTCAGGTGGGAACTGGCTCATGGAGGAA
ACTAAGAGCGGCGTCGCAGCTTCTGGTGAAGGTGCCACGTGGACGGCGGCAGAGAACAAG
GCATTCGAGAATGCTTTGGCGGTTTACGACGACAACACTCCTGATCGGTGGCAGAAGGTG
GCTGCGGTGATTCCGGGGAAGACAGTGAGTGACGTAATTAGACAGTATAACGATTTGGAA
GCTGATGTCAGCAGCATCGAGGCCGGTTTAATCCCGGTCCCCGGTTACATCACCTCGCCG
CCTTTCACTCTAGATTGGGCCGGCGGCGGTGGCGGATGTAACGGGTTTAAACCGGGTCAT
CAGGTTTGTAATAAACGGTCGCAGGCCGGTAGATCGCCGGAGCTGGAGCGGAAGAAAGGC
GTTCCTTGGACGGAGGAAGAACACAAGCTATTTCTAATGGGTTTGAAGAAATATGGGAAA
GGAGATTGGAGAAACATATCTCGGAACTTTGTGATAACGCGAACGCCAACACAAGTAGCT
AGCCACGCCCAAAAGTACTTCATCCGGCAACTTTCCGGCGGCAAGGACAAGAGACGAGCA

AGCATTCACGACATAACCACCGTAAATCTCGAAGAGGAGGCTTCTTTGGAGACCAATAAG
AGCTCCATTGTTGTTGGAGATCAGCGTTCAAGGCTAACCGCGTTTCCTTGGAACCAAACG
GACAACAATGGAACACAGGCAGACGCTTTCAATATAACGATTGGAAACGCTATTAGTGGC
GTTCATTCATACGGCCAGGTTATGATTGGAGGGTATAACAATGCAGATTCTTGCTATGAC
GCCCAAAACACAATGTTTCAACTATAG
>G1641 Amino Acid Sequence (domain in AA coordinates: 139-200)
MEVMRPSTSHVSGGNWLMEETKSGVAASGEGATWTAAENKAFENALAVYDDNTPDRWQKV
AAVIPGKTVSDVIRQYNDLEADVSSIEAGLIPVPGYITSPPFTLDWAGGGGGCNGFKPGH
QVCNKRSQAGRSPELERKKGVPWTEEEHKLFLMGLKKYGKGDWRNISRNFVITRTPTQVA
SHAQKYFIRQLSGGKDKRRASIHDITTVNLEEEASLETNKSSIVVGDQRSRLTAFPWNQT
DNNGTQADAFNITIGNAISGVHSYGQVMIGGYNNADSCYDAQNTMFQL*
>G165 (19..699)
CTTCAAAACATCTAAAAAATGGTGAAAAAAACTCTTGGTCGTAGAAAGGTAGAGATAGTG
AAAATGACTAAGGAATCAAACCTTCAAGTCACATTTTCCAAGAGAAAAGCTGGTCTTTTT
AAGAAGGCTAGTGAATTTTGCACATTATGTGATGCAAAAATTGCGATGATCGTGTTTTCA
CCAGCTGGAAAAGTATTTTCTTTTGGTCATCCAAATGTTGATGTTCTGCTTGACCACTTT
CGAGGGTGTGTTGTAGGACACAACAACACAAACCTTGATGAAAGCTACACAAAGCTTCAT
GTTCAAATGCTCAACAAATCCTACACTGAGGTGAAGGCGGAAGTAGAAAAAGAACAAAAG
AATAAGCAGTCGCGGGCTCAAAATGAAAGAGAAAACGAAAACGCTGAGGAGTGGTGGAGT
AAGTCTCCATTAGAACTCAACTTAAGTCAATCAACCTGTATGATACGTGTTCTTAAAGAT
TTGAAGAAGATAGTTGATGAAAAAGCAATTCAATTAATCCATCAAACAAACCCAAACTTC
TATGTTGGAAGTTCTAGCAATGCTGCTGCTCCAGCAACTGTTAGTGGTGGTAATATCTCC
ACAAACCAGGGGTTCTTTGATCAAAACGGAATGACGACTAATCCTACTCAAACACTTCTG
TTTGGATTTGATATTATGAATCGCACACCAGGAGTTTAAATAAGTCTATCCTCATTATGG
GTCTTGGTACTATAAGTTCATCTCTCTCGTTGTTGACTTTTTAAGTCTCCAATAGTTTGT
TGTG
>G165 Amino Acid Sequence (conserved domain in AA coordinates:7-62)
MVKKTLGRRKVEIVKMTKESNLQVTFSKRKAGLFKKASEFCTLCDAKIAMIVFSPAGKVF
SFGHPNVDVLLDHFRGCVVGHNNTNLDESYTKLHVQMLNKSYTEVKAEVEKEQKNKQSRA
QNERENENAEEWWSKSPLELNLSQSTCMIRVLKDLKKIVDEKAIQLIHQTNPNFYVGSSS
NAAAPATVSGGNISTNQGFFDQNGMTTNPTQTLLFGFDIMNRTPGV*
>G1652 (77..1078)
AGCAAGTCCAAATCTCCCTCTCTCTCTCTCTATCTATCTCTCTATAGAAGATTTTTTAAC
TAAGAAGCTAGCGATCATGGCCACAGCGATGAACGTTTTCTCTACCAAATGGTCCTCCGA
ATTGGATATAGAAGAATATAGTATCATCCACCAATTCCACATGAACTCACTCGTCGGAGA
TGTTCCACAGTCTCTCTCATCTCTTGATGATACCACCACTTGTTATAACCTTGATGCTTC
TTGTAATAAAAGTTTGGTAGAAGAAAGACCTTCAAAGATCCTCAAGACCACTCACATATC
ACCAAACTTACATCCTTTTTCTTCTTCTAATCCTCCTCCTCCAAAGCACCAGCCCTCTTC
TAGGATTCTTTCTTTTGAAAAGACAGGTTTACATGTTATGAATCACAACTCTCCAAACTT
AATATTTAGCCCCAAGGACGAAGAAATTGGATTACCAGAGCATAAGAAAGCCGAGCTGAT
AATAAGAGGGACAAAGAGAGCTCAATCCTTGACTCGAAGCCAATCAAATGCTCAAGATCA
CATACTGGCAGAGAGAAAACGGAGAGAGAAGCTTACTCAAAGATTTGTAGCTCTTTCCGC
GCTAATTCCTGGCCTAAAGAAGATGGACAAGGCTTCTGTGTTGGGAGATGCAATAAAGCA
TATAAAGTACCTCCAAGAGAGTGTGAAAGAGTATGAGGAACAAAAGAAGGAAAAGACAAT
GGAATCAGTGGTTCTTGTAAAGAAGTCTAGTCTGGTTTTAGATGAAAATCATCAACCATC
ATCATCATCTTCCTCAGATGGAAATCGCAATAGCTCGAGCTCAAATCTTCCAGAAATAGA
AGTTAGGGTTTCAGGAAAAGATGTTCTTATTAAGATCCTATGCGAGAAGCAAAAGGGTAA
TGTGATCAAGATTATGGGGGAGATTGAAAAGCTTGGTTTGTCTATCACCAACAGCAATGT
CTTGCCCTTTGGACCCACTTTTGACATCTCTATTATCGCTCAGAAGAATAACAATTTTGA
TATGAAAATCGAGGATGTTGTGAAGAACTTGAGTTTTGGCTTATCAAAGCTCACTTAATT
GGTTTCACGTTACATACATATACACATTCATCATCGATTTCTCCGATCGAAGAATCCAAA
ATCAGTTTTTCCATGAAAGTGGTTTTTTAGTTGTTAAGTTTGTATGGAGATTCTTAA
GTCATTTAAAGATCCTTGTTCTTGTGTTGTTAAGTGTGCTTTAAGATGCATATCATCAAA
TGTTTAGTAATTATTTCTCTCCAGTTTCATTTGGACGGAATTTTTTTCGCAGTTGTTGG
ATATATATTTCCTGCGATGTAAAGCATTTCGTTAGTTTAATAAACGTCCGATATGTTTCT
TTGAAAA
>G1652 Amino Acid Sequence (domain in AA coordinates:143-215)

MATAMNVFSTKWSSELDIEEYSIIHQFHMNSLVGDVPQSLSSLDDTTTCYNLDASCNKSL
VEERPSKILKTTHISPNLHPFSSSNPPPPKHQPSSRILSFEKTGLHVMNHNSPNLIFSPK
DEEIGLPEHKKAELIIRGTKRAQSLTRSQSNAQDHILAERKRREKLTQRFVALSALIPGL
KKMDKASVLGDAIKHIKYLQESVKEYEEQKKEKTMESVVLVKKSSLVLDENHQPSSSSS
DGNRNSSSSNLPEIEVRVSGKDVLIKILCEKQKGNVIKIMGEIEKLGLSITNSNVLPFGP
TFDISIIAQKNNNFDMKIEDVVKNLSFGLSKLT*
>G1655 (132..755)
TTTCTAACTAGTCACATTGAGAGAGAGAGAGAGAGAAAGAGAGACTCTCAGAATCTGAAG
AAGAAGAAGAGATTGTTGTTTTTGCCTTTTATCATCGGTTTCTTTGAATCTCTGGTTTTA
AATCGGATTTAATGGTGGAGTCTCTGTTCCCGAGCATCGAAAACACAGGTGAATCGTCTC
GAAGAAAGAAGCCGAGGATATCAGAGACGGCGGAGGCGGAGATAGAGGCACGACGTGTCA
ACGAAGAAAGCTTGAAGAGATGGAAAACGAATCGTGTGCAACAGATCTACGCTTGTAAGC
TCGTCGAAGCTTTACGCCGAGTTCGTCAGAGATCTTCCACCACCAGCAACAACGAGACCG
ATAAACTCGTCTCCGGCGCGGCGAGGGAGATACGTGATACGGCGGATCGAGTTCTAGCTG
CGTCCGCTCGTGGTACGACTCGGTGGAGCAGAGCGATTTTAGCGAGTCGCGTCCGAGCGA
AGCTGAAGAAACATAGAAAGGCGAAAAAGTCAACGGGAAATTGTAAATCGAGAAAAGGTC
TCACGGAGACGAATCGGATTAAGTTACCGGCGGTTGAGAGAAAACTGAAGATTCTTGGCC
GTTTGGTTCCTGGTTGCCGGAAAGTCTCTGTACCGAATCTTTTAGATGAAGCGACCGATT
ACATCGCAGCGTTAGAGATGCAGGTTCGAGCCATGGAGGCTCTCGCCGAACTTTTAACCG
CAGCCGCACCACGGACGACGTTGACCGGAACTTAACGGCGGCAGTTAGTTTGTCAGTTGT
TAATTAGCTTTTCTTTTACCTTTTTACCCCTTTATTTTGGCTTCAAGTGTTTTTTTTTC
TCGTCGACGCGATTTTAATTTATTAAATTCA
>G1655 Amino Acid Sequence (domain in AA coordinates: 134-192)
MVESLFPSIENTGESSRRKKPRISETAEAEIEARRVNEESLKRWKTNRVQQIYACKLVEA
LRRVRQRSSTTSNNETDKLVSGAAREIRDTADRVLAASARGTTRWSRAILASRVRAKLKK
HRKAKKSTGNCKSRKGLTETNRIKLPAVERKLKILGRLVPGCRKVSVPNLLDEATDYIAA
LEMQVRAMEALAELLTAAAPRTTLTGT*
>G1671 (188..751)
TCCCACTATCCTTCGCAAGACCCTTCCTCTATATAAGGAAGTTCATTTCATTTGGAGAGG
ACACGCTGACAAGCTGACTCTAGCAGATCTGGTACCGTCGACCCTCTCTATATAATCTTC
TTCTACACACACACACACACGCAACCATATACGTACATGTGAAGTAGTGAGATCAATATC
GTTAGCAATGAATCTACCACCGGGATTTAGGTTTTTTCCGACCGATGAAGAGCTCGTCGT
TCACTTCCTCCACCGGAAAGCTTCCCTCTTGCCTTGTCACCCTGATGTCATCCCCGACCT
TGATCTTTACCATTACGATCCTTGGGACCTTCCCGGGAAAGCTTTGGGAGAAGGGAGGCA
ATGGTACTTCTATAGTAGAAAGACACAAGAGAGAGTGACAAGCAATGGGTATTGGGGATC
AATGGGAATGGACGAGCCAATCTACACAAGCTCCACACACAAGAAAGTGGGAATCAAAAA
GTATCTAACTTTCTATCTCGGAGATTCTCAGACTAATTGGATCATGCAAGAATATTCCCT
CCCGGATTCCTCTTCTTCATCTAGTCGATCTTCTAAGAGATCAAGCCGTGCTTCTAGTTC
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CGGATCCTCTAGCTAGAGCTTTCGTTCGTATCATCGGTTTCGACAACGTTCGTCAAGT
>G1671 Amino Acid Sequence (domain in AA coordinates: TBD)
MNLPPGFRFFPTDEELVVHFLHRKASLLPCHPDVIPDLDLYHYDPWDLPGKALGEGRQWY
FYSRKTQERVTSNGYWGSMGMDEPIYTSSTHKKVGIKKYLTFYLGDSQTNWIMQEYSLPD
SSSSSSRSSKRSSRASSSSHKPDYSKWVICRVYEQNCSEEEDDDGTELSCLDEVFLSLDD
LDEVSLP*
>G1756 (71..1003)
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AGGCTACTCCGGCTCCGGAGACGCGTTTTCCGGCGAAAGTTCCGGTACGTTTTCACCTTC
GTTTTGCCTACCGATGGAGACGTCTAGTTTCTACGAACCGGAGATGGAGACAAGTGGCTT
AGATGAGCTCGGTGAACTTTACAAACCCCTTTTACCCTTTCTCCACACAAACGATCCTCAC
AAGCTCGGTCTCTCTCCCTGAAGATTCAAAACCTTTCCGAGATGACAAGAAACAACGATC
ACATGGTTGTCTTTTATCCAACGGATCAAGAGCTGATCATATCCGAATTTCAGAATCCAA
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TCTGTTGTCGGACGCATGGGCGTGGCGTAAATACGGGCAGAAACCCATCAAAGGATCTCC
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CGAAAGAAATCCTCAAAACCCGGAGAAATTCACCATAACATACACTAATGAGCACAATCA
TGAACTACCAACCCGGAGAAACTCATTAGCCGGTTCGACTCGAGCAAAAACTTCCCAACC
CAAACCAACCTTAACCAAAAAATCCGAAAAAGAAGTTGTTTCTTCCCCTACAAGTAATCC
TATGATCCCATCCGCTGATGAATCTTCTGTTGCGGTTCAAGAAATGAGCGTTGCGGAAAC
GAGTACGCACCAAGCGGCTGGAGCAATCGAGGGCCGCCGCTTGAGTAACGGTTTACCATC
GGATTTGATGTCCGGGAGCGGAACTTTTCCAAGTTTTACCGGTGACTTCGATGAACTATT
GAATAGCCAAGAGTTCTTCAGTGGGTATTTATGGAATTACTAGAGAGCATTAGGTGTATG
TATATATATAT

>G1756 Amino Acid Sequence (domain in AA coordinates: TBD)
MGEVAYMDEGDLEAIVRGYSGSGDAFSGESSGTFSPSFCLPMETSSFYEPEMETSGLDEL
GELYKPFYPFSTQTILTSSVSLPEDSKPFRDDKKQRSHGCLLSNGSRADHIRISESKSKK
SKKNQQKRVVEQVKEENLLSDAWAWRKYGQKPIKGSPYPRSYYRCSSSKGCLARKQVERN
PQNPEKFTITYTNEHNHELPTRRNSLAGSTRAKTSQPKPTLTKKSEKEVVSSPTSNPMIP
SADESSVAVQEMSVAETSTHQAAGAIEGRRLSNGLPSDLMSGSGTFPSFTGDFDELLNSQ
EFFSGYLWNY*

>G1757 (250..1224)
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>G1757 Amino Acid Sequence (domain in AA coordinates: 158-218)
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ESHHRQDYIFNSKKRKMLPKWSEKVRISPERGLEGPQDDVFSWRKYGQKDILGAKFPRSY
YRCTHRSTQNCWATKQVQRSDGDATVFEVTYRGTHTCSQAITRTPPLASPEKRQDTRVKP
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VDWFNPTVEIDTTFPAFLHESIYY*

>G1782 (1..927)
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>G1782 Amino Acid Sequence (domain in AA coordinates: 166-238)
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>G184 (327..1937)
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>G184 Amino Acid Sequence (domain in AA coordinates: 295-352)
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>G1845 (111..989)
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>G1845 Amino Acid Sequence (domain in AA coordinates: 140-207)
MDFDEELNLCITKGKNVDHSFGGEASSTSPRSMKKMKSPSRPKPYFQSSSSPYSLEAFPF
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PRGRMMMMMSQEAVQPYIATKLYRGVRQRQWGKWVAEIRKPRSRARLWLGTFDTAEEAAM
AYDRQAFKLRGHSATLNFPEHFVNKESELHDSNSSDQKEPETPQPSEVNLESKELPVIDV
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>G1879 (3..917)
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>G1879 Amino Acid Sequence (domain in AA coordinates: 107-176)
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KGDKTSTSSLVGPFTDFFSFPQYSTKSSSDVPESSSSPAEIEVTVAESHANIKIMTKKKP
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QEET*
>G1888 (1..729)
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>G1888 Amino Acid Sequence (domain in aa coordinates: 5-50)
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>G189 (34..987)
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>G189 Amino Acid Sequence (domain in AA coordinates: 240-297)
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>G1939 (92..844)
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>G1939 Amino Acid Sequence (domain in AA coordinates: 40-102)
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GSDRREEDPR*
>G194 (192..1205)
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>G194 Amino Acid Sequence (domain in AA coordinates: 174-230)
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>G1943 (137..1858)
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ACCAATGGTTCAACATGGAAAGAGTTCATATGTATCTAGTTTTGTTGAGATGATGTCGAC
GGGACAGGGTATGATGTCGCCAATGATGAATGCCGGGAATACGCAACAGTTCATGCCCCA
TATGGCCATGGATATGAACCGACCTCCTCCATTCATACCTTTCCCCGGCACATCTTTTCC
TATGCCGGCTCAAATGGCAGGTGTAGGTCCATCATATCCAGCACCGCGCTACCCTTTTCC
CAACATTCAGACCTTTGACCCATCCAGAGTCCGTTTACCAAGCCCGCAGCCTAACCCGGT
GTCGAACCAGCCTCAGTTTCCGGCTTACATGAATCCCTATAGCCAGTTTGCTGGTCCCCA
CCAGTTGCAACAACCTCCTCCTCCTCCATTTCAGGGTCAAACAACATCACAACTGAGTTC
CGGGCAGGCAAGTAGTAGCAAGGAACCTGAGGATCAGGAGAACCAACCAACAGCTTAGTT
AAAGTGTGGAGCTGAAACGGATCAGTTCTTCAAGCAAATTACAACTTTGAAGATAAACCA
GAGTTGTAACATGTAGATTTTGTCTGTTAAGTTTAATGTAAGTACTTTTTAGTTAATGGG
AAAGATACTGACAGGTTGCAAGGTGGTCAGTATTTGTGCATCACGCTTAAGATTCCTCGA
TGTGGCCAGTATCTCCCTTTTCTAGCATGTGAGGTCCCTACTCTCTGGTTCTACGGAGAC
CAAATGTTCGACTGATTAAACACACAATGACTTACCAAAAGTACACGCGGCCCATCCTCG
TCTTTATGTTCCAAGTGCGACTGTTTGTTTATTTGTAAGCATTTTTCTTATAATAATAAA
ACAGCTCTATCTTCGTTAAAAAAAA

>G1943 Amino Acid Sequence (domain in AA coordinates: 335-406)

MGEDDIVELLWKSGQVVRTSQTQRPSSNTPPSLPPPPILRGSGSGNGEENAPLPLPQPSP
PLHHQNLFILEDEMSSWLHHSHPGVTSTPASSVSLPPPPNAPREDDIVELLWQSGQVVGT
NQTHRQSYDPPPILRGSGSGRGEENAPLSQPPPHLHQQNLFIQEGEMYSWLHHSYRQNYF
CSELLNSTPATHPQSSISLAPRQTIATRRAENFMNFSWLRGNIFTGGRVDEAGPSFSVVR
ESMQVGSNTTPPSSSATESCVIPATEGTASRVSGTLAAHDLGRKGKAVAVEAAGTPSSGV
CKAETEPVQIQPATESKLKAREETHGTEEARGSTSRKRSRTAEMHNLAERRRREKINEKM
KTLQQLIPRCNKVESDSVSTLISLLKFQRWMMLSSTSNRYRAKYKYALQNRMCFKPMVQH
GKSSYVSSFVEMMSTGQGMMSPMMNAGNTQQFMPHMAMDMNRPPPFIPFPGTSFPMPAQM
AGVGPSYPAPRYPFPNIQTFDPSRVRLPSPQPNPVSNQPQFPAYMNPYSQFAGPHQLQQP
PPPPFQGQTTSQLSSGQASSSKEPEDQENQPTA*

>G21 (79..966)

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GCTTCTTCTCTCATAACAATGGCAAGACAAATCAACATAGAGAGTAGTGTTTCTCAAGTT
ACCTTTATCTCCTCCGCCATCCCCGCCGTATCTTCCTCCTCCTCCATCACCGCTTCCGCC
TCATTGTCCTCTTCACCTACTACATCTTCCTCTTCTTCGTCATCAACAAATTCTAACTTC
ATTGAGGAAGACAACTCTAAAAGAAAAGCATCTCGAAGATCATTGTCATCGTTAGTCTCC
GTTGAAGACGATGATGATCAAAACGGTGGAGGTGGGAAACGGCGAAAGACCAACGGTGGA
GATAAACATCCGACGTATAGAGGAGTGAGGATGAGGAGTTGGGGAAAATGGGTGTCGGAG
ATTAGAGAGCCGAGAAAGAAATCAAGAATCTGGCTCGGGACTTATCCAACGGCTGAGATG
GCAGCTCGAGCTCATGACGTAGCGGCTTTAGCCATTAAAGGTACAACGGCTTACCTCAAT
TTTCCCAAGTTAGCCGGCGAGCTTCCTCGTCCAGTCACAAATTCTCCTAAAGACATTCAA
GCCGCCGCCTCTTTAGCGGCCGTTAACTGGCAAGATTCGGTCAACGATGTGAGTAATTCT
GAAGTGGCTGAAATAGTTGAAGCCGAGCCGAGTCGAGCCGTGGTGGCTCAGTTGTTTTCT
TCGGACACAAGCACGACGACGACGACTCAGAGTCAAGAGTATTCGGAAGCTTCGTGTGCT

TCGACTTCGGCGTGTACGGACAAAGACAGTGAGGAAGAGAAGCTGTTTGATTTGCCGGAT
TTGTTTACCGATGAGAATGAGATGATGATACGAAACGATGCGTTTTGCTACTACTCGTCC
ACGTGGCAGCTTTGTGGAGCCGATGCTGGGTTTCGGCTTGAAGAGCCGTTTTTTCTATCT
GAATGACTAAAGTACCCCTCTCGAGAGAGCTCTCACTAACACT
>G21 Amino Acid Sequence (domain in AA coordinates: 97-164)
MARQINIESSVSQVTFISSAIPAVSSSSSITASASLSSSPTTSSSSSSSTNSNFIEEDNS
KRKASRRSLSSLVSVEDDDDQNGGGGKRRKTNGGDKHPTYRGVRMRSWGKWVSEIREPRK
KSRIWLGTYPTAEMAARAHDVAALAIKGTTAYLNFPKLAGELPRPVTNSPKDIQAAASLA
AVNWQDSVNDVSNSEVAEIVEAEPSRAVVAQLFSSDTSTTTTTQSQEYSEASCASTSACT
DKDSEEEKLFDLPDLFTDENEMMIRNDAFCYYSSTWQLCGADAGFRLEEPFFLSE*
>G2132 (42..1031)
ATTCTGTTACTTAGTACCGGAGTTTAGTCGGAGAGAGAACAATGATCAGTTTCAGAGAAG
AGAACATCGATCTCAACTTGATTAAAACAATTAGTGTAATCTGTAATGATCCAGACGCCA
CCGATTCCTCTAGCGACGATGAATCTATCTCCGGCAATAATCCTCGCCGTCAGATCAAAC
CAAAACCACCGAAACGTTACGTCTCAAAGATCTGTGTCCCGACGCTGATCAAAAGGTATG
AGAACGTTTCGAATTCTACAGGGAATAAAGCAGCCGGAAACCGGAAAACGTCGTCGGGTT
TCAAAGGCGTACGACGGAGGCCGTGGGGGAAATTTGCGGCGGAGATAAGAAATCCGTTTG
AGAAGAAGAGAAAGTGGCTTGGAACGTTTCCTACTGAAGAAGAAGCAGCAGAAGCTTACC
AAAAGAGTAAAAGAGAGTTTGATGAACGATTGGGTTTAGTTAAACAGGAAAAAGACCTAG
TAGATTTGACCAAGCCGTGCGGTGTACGTAAACCAGAAGAGAAGGAAGTTACTGAGAAGT
CGAATTGCAAAAAGGTAAATAAGAGAATTGTTACTGATCAGAAGCCATTTGGTTGTGGTT
ATAACGCTGATCATGAAGAAGAGGGAGTGATTAGTAAAATGTTGGAAGATCCGTTGATGA
CATCGTCAATTGCTGATATTTTTGGTGATTCGGCTGTTGAAGCAAATGATATTTGGGTGG
ATTACAATTCAGTGGAATTTATTTCCATTGTAGATGATTTCAAGTTTGATTTTGTGGAGA
ATGATAGAGTAGGAAAGGAGAAAACATTTGGATTTAAGATTGGGGATCACACTAAAGTTA
ATCAACATGCCAAAATCGTATCGACCAATGGGGACTTATTCGTCGATGATTTACTTGATT
TTGATCCGTTGATAGATGATTTTAAGTTAGAAGATTTTCCTATGGATGATCTTGGATTAT
TAGGAGATCCAGAGGATGATGATTTTAGTTGGTTTAATGGTACTACTGATTGGATCGATA
AGTTTTTATGAATACTTTCTTGACACGGCCAACGGTATTAGTAC
>G2132 Amino Acid Sequence (domain in AA coordinates: TBD)
MISFREENIDLNLIKTISVICNDPDATDSSSDDESISGNNPRRQIKPKPPKRYVSKICVP
TLIKRYENVSNSTGNKAAGNRKTSSGFKGVRRRPWGKFAAEIRNPFEKKRKWLGTFPTEE
EAAEAYQKSKREFDERLGLVKQEKDLVDLTKPCGVRKPEEKEVTEKSNCKKVNKRIVTDQ
KPFGCGYNADHEEEGVISKMLEDPLMTSSIADIFGDSAVEANDIWVDYNSVEFISIVDDF
KFDFVENDRVGKEKTFGFKIGDHTKVNQHAKIVSTNGDLFVDDLLDFDPLIDDFKLEDFP
MDDLGLLGDPEDDDFSWFNGTTDWIDKFL*
>G2145 (1..777)
ATGGACGTTTTTGTTGATGGTGAATTGGAGTCTCTCTTGGGGATGTTCAACTTTGATCAA
TGTTCATCATCTAAAGAGGAGAGACCGCGAGACGAGTTGCTTGGCCTCTCTAGCCTTTAC
AATGGTCATCTTCATCAACATCAACACCATAACAATGTCTTATCTTCTGATCATCATGCT
TTCTTGCTCCCTGATATGTTCCCATTTGGTGCAATGCCGGGAGGAAATCTTCCGGCCATG
CTTGATTCTTGGGATCAAAGTCATCACCTCCAAGAAACGTCTTCTCTTAAGAGGAAACTA
CTTGACGTGGAGAATCTATGCAAAACTAACTCTAACTGTGACGTCACAAGACAAGAGCTT
GCGAAATCCAAGAAAAAACAGAGGGTAAGCTCGGAAAGCAATACAGTTGACGAGAGCAAC
ACTAATTGGGTAGATGGTCAGAGTTTAAGCAACAGTTCAGATGATGAGAAAGCTTCGGTC
ACAAGTGTTAAAGGCAAAACTAGAGCCACCAAAGGGACAGCCACTGATCCTCAAAGCCTT
TATGCTCGGAAACGAAGAGAGAAGATTAACGAAAGGCTCAAGACACTACAAAACCTTGTG
CCAAACGGGACAAAAGTCGATATAAGCACGATGCTTGAAGAAGCGGTCCATTACGTGAAG
TTCTTGCAGCTTCAGATTAAGTTGTTGAGCTCGGATGATCTATGGATGTACGCACCATTG
GCTTACAACGGCCTGGACATGGGGTTCCATCACAACCTTTTGTCTCGGCTTATGTGA
>G2145 Amino Acid Sequence (domain in AA coordinates:166-243)
MDVFVDGELESLLGMFNFDQCSSSKEERPRDELLGLSSLYNGHLHQHQHHNNVLSSDHHA
FLLPDMFPFGAMPGGNLPAMLDSWDQSHHLQETSSLKRKLLDVENLCKTNSNCDVTRQEL
AKSKKKQRVSSESNTVDESNTNWVDGQSLSNSSDDEKASVTSVKGKTRATKGTATDPQSL
YARKRREKINERLKTLQNLVPNGTKVDISTMLEEAVHYVKFLQLQIKLLSSDDLWMYAPL
AYNGLDMGFHHNLLSRLM*
>G23 (22..732)

TATCAAACGAGAGTACAAAAGATGACGTCACTCAACAGCTCTGCATCACCAACATCATCG
TCATCAGACCAATCTGATGCAACTACTACAACAAGCACCCACTTGTCTGAAGAAGAAGCT
CCACCCAGAAACAACAACACAAGAAAGAGAAGGAGAGATTCTTCTTCTGCTTCTTCATCT
TCTTCAATGCAACATCCTGTTTACAGAGGTGTGCGGATGAGAAGTTGGGGCAAATGGGTC
TCCGAGATCCGACAACCTCGTAAGAAAACTCGTATTTGGCTCGGCACTTTTGTCACCGCT
GATATGGCTGCTCGTGCTCACGACGTCGCTGCTCTCACCATCAAAGGCTCCTCCGCCGTC
TTAAATTTCCCTGAGCTTGCTTCTCTCTTCCCTCGTCCGGCGTCATCATCGCCGCATGAT
ATCCAGACAGCCGCCGCAGAAGCCGCCGCCATGGTGGTCGAAGAAAAACTGTTAGAGAAG
GATGAGGCTCCGGAGGCCCCACCTTCGTCGGAATCTTCTTACGTGGCGGCGGAGTCAGAG
GATGAGGAGAGGTTGGAGAAAATTGTGGAGCTGCCTAACATTGAAGAAGGAAGTTATGAC
GAGAGTGTGACATCACGTGCTGATCTGGCTTATTCTGAGCCGTTCGATTGTTGGGTGTAT
CCTCCGGTTATGGATTTTTATGAAGAAATATCGGAGTTTAATTTCGTGGAATTGTGGAGC
TTTAATCACTAATTAAGTTAGGAAAGTGCATTATATTGCAATATTGCATCATAGATAACA
TTTGTATTTCTTTTCTTTTTGTACGGATACGTAGCATATGCTACTATACTAGGGCTAGTG
TACCAAATATTGTAAAATATACTTATTAATATTTATGTAAATGTGTAATATATATATAACAT
ACAATTATTGTAAGTTTGGAAATTGGAAACTATCGTTACGCAATGTTCTTGTAAAAAAAA
AAAAAAAAAA

>G23 Amino Acid Sequence (domain in AA coordinates: 61-117)
MTSLNSSASPTSSSSDQSDATTTTSTHLSEEEAPPRNNNTRKRRRDSSSASSSSSMQHPV
YRGVRMRSWGKWVSEIRQPRKKTRIWLGTFVTADMAARAHDVAALTIKGSSAVLNFPELA
SLFPRPASSSPHDIQTAAAEAAAMVVEEKLLEKDEAPEAPPSSESSYVAAESEDEERLEK
IVELPNIEEGSYDESVTSRADLAYSEPFDCWVYPPVMDFYEEISEFNFVELWSFNH*

>G2313 (104..724)
CGTCGACACAATCGCTCTTCCGTAACATATTCCACAAAACGATCTTCTTGTTTCTTGAAT
TTTTAGCCATCTCTTTTTTTTTTTTTCTCATTTTCTCGGATACTATGGCTTCGAGTCCACG
CTGGACGGAGGACGACAACAGGCGTTTTAAGTCAGCTCTGTCGCAATTCCCTCCGGATAA
CAAGCGTTTGGTGAATGTCGCCCAGCATCTGCCGAAACCTTTGGAGGAGGTGAAGTACTA
CTACGAAAAGTTGGTCAACGATGTTTATCTGCCGAAACCTTTAGAGAATGTCACCCAGCA
TCTGCAGAAACCTATGGAAATGGAGGAGATGAAGTACATGTACGAAAAGATGGCCAACGA
TGTTAATCAGATGCCCGAGTACGTACCACTGGCGGAATCGAGTCAGTCCAAACGCAGGAA
GAAGGATACGCCAAATCCTTGGACAGAAGAGGAACACAGATTGTTTCTGCAAGGATTGAA
AAAGTATGGGGAAGGAGCTTCGACGTTGACATCAACGAATTTTGTGAAGACAAAGACTCC
ACGGCAAGTGTCAAGCCATGCACAGTATTACAAAAGGCAAAAATCGGACAATAAGAAGGA
GAAACGCCGGAGTATTTTTGACATAACTTTGGAGTCTACCGAGGGCAATCCAGATTCTGG
AAATCAGAACCCTCCGGATGATGATGATCCGTCCCAAGGTCAAGGCACTTGTCTTGGAGT
TTAGATGTTGGAAGATAGAAGAATGGTGTGAAAGC

>G2313 Amino Acid Sequence (domain in AA coordinates: TBD)
MASSPRWTEDDNRRFKSALSQFPPDNKRLVNVAQHLPKPLEEVKYYYEKLVNDVYLPKPL
ENVTQHLQKPMEMEEMKYMYEKMANDVNQMPEYVPLAESSQSKRRKKDTPNPWTEEEHRL
FLQGLKKYGEGASTLTSTNFVKTKTPRQVSSHAQYYKRQKSDNKKEKRRSIFDITLESTE
GNPDSGNQNPPDDDDPSQGQGTCLGV*

>G2344 (1..573)
ATGACTTCTTCAATCCATGAGCTTTCTGATAACATTGGAAGTCATGAGAAGCAAGAACAG
AGAGATTCTCATTTCCAACCACCAATCCCTTCTGCAAGAAATTATGAATCAATTGTTACA
AGTTTAGTCTACTCAGACCCGGGGACTACAAATTCCATGGCACCTGGACAATATCCATAT
CCAGATCCTTACTACAGAAGCATATTTGCACCGCCTCCACAACCGTATACCGGGGTACAT
CTACAGTTGATGGGAGTGCAGCAACAAGGCGTTCCTTTACCATCTGATGCAGTCGAGGAA
CCTGTTTTTGTTAACGCAAAGCAATACCACGGTATACTAAGGCGCAGACAATCAAGAGCA
AGACTTGAGTCTCAGAATAAAGTCATCAAGTCACGTAAGCCGTATTTGCATGAATCTCGG
CATTTGCATGCGATAAGACGACCAAGAGGATGTGGCGGGCGGTTTCTAAATGCCAAGAAG
GAGGATGAGCATCACGAAGACAGTAGTCATGAAGAAAAATCCAACCTTAGCGCTGGTAAA
TCCGCCATGGCTGCTTCTAGTGGTACATCTTGA

>G2344 Amino Acid Sequence (domain in AA coordinates: TBD)
MTSSIHELSDNIGSHEKQEQRDSHFQPPIPSARNYESIVTSLVYSDPGTTNSMAPGQYPY
PDPYYRSIFAPPPQPYTGVHLQLMGVQQQGVPLPSDAVEEPVFVNAKQYHGILRRRQSRA
RLESQNKVIKSRKPYLHESRHLHAIRRPRGCGGRFLNAKKEDEHHEDSSHEEKSNLSAGK
SAMAASSGTS*

>G2430 (69..1907)
AACTTCAACATACACATAATCTCTCACTTAAAAATATCTCTCTCTCTCTCTACAAAAT
CAATTCCAATGTTGGTGGGAAAGATAAGTGGATATGAAGATAATACTCGCTCTTTGGAGC
GAGAAACATCTGAAATCACTTCTCTTCTCAGCCAATTTCCGGGGAATACTAATGTCCTTG
TTGTTGACACCAATTTCACCACTCTACTCAACATGAAACAAATCATGAAACAATACGCTT
ATCAAGTGTCTATTGAGACAGATGCAGAAAAAGCTCTTGCGTTTTTGACAAGCTGCAAAC
ATGAAATCAATATTGTGATTTGGGATTTTCATATGCCTGGAATTGATGGACTTCAAGCTC
TCAAGAGCATTACTTCAAAGTTGGATTTACCTGTAGTGATTATGTCTGATGATAATCAAA
CGGAATCTGTGATGAAAGCAACATTTTACGGTGCTTGTGACTATGTTGTGAAACCGGTTA
AAGAAGAGGTAATGGCCAATATATGGCAACACATTGTACGGAAGAGGCTGATCTTTAAAC
CGGATGTTGCTCCACCGGTTCAATCAGATCCGGCTCGCTCTGACCGTTTAGACCAAGTCA
AAGCTGATTTCAAGATCGTAGAAGATGAACCAATAATCAATGAGACACCGCTGATCACAT
GGACCGAAGAAATTCAACCGGTTCAGTCAGATCTGGTTCAAGCCAACAAGTTCGACCAAG
TGAATGGCTATTCCCCAATCATGAACCAAGATAACATGTTCAACAAAGCACCACCTAAAC
CGCGAATGACGTGGACAGAAGTTATTCAACCGGTTCAATCAAATCTGGTTCAAACAAAAG
AGTTCGGCCAACTCAATGACTATTCCCAAATCATGAACCAAGATAGCATGTACAACAAAG
CAGCAACCAAACCACAATTGACGTGGACCGAAGAAATTCAACCGGTTCAATCAGGTCTGG
TTCAAGCCAACGAGTTCAGCAAAGTGAATGGATATTCCCAAAGCATGAACCAAGATAGCA
TGTTCAACAAATCAGCAACCAACCCGCGATTGACATGGAACGAATTACTTCAACCGGTTC
AATCAGATCTGGTTCAATCCAATGAGTTTAGCCAATTCAGTGACTATTCTCAAATCATGA
ACGAAGATAACATGTTCAACAAAGCAGCAAAGAAACCGCGGATGACATGGAGTGAAGTAT
TTCAACCGGTTCAATCACATCTGGTTCCGACTGACGGTTTAGACCGAGACCACTTTGATT
CCATAACCATAAACGGAGGTAACGGCATACAAAACATGGAAAAGAAACAAGGAAAAAAAC
CACGGAAGCCGCGGATGACGTGGACCGAAGAGCTTCACCAAAAATTTCTGGAAGCCATCG
AAATAATTGGTGGTATCGAAAAAGCTAACCCAAAGGTACTTGTCGAATGCTTGCAAGAAA
TGAGGATAGAAGGAATTACTAGAAGCAATGTGGCAAGTCATCTTCAGAAACACCGTATCA
ATCTTGAAGAAAACCAAATTCCTCAACAAACACAAGGGAATGGTTGGGCCACTGCGTATG
GTACACTAGCTCCCTCTCTCCAAGGTTCAGACAATGTCAACACAACAATACCATCGTACC
TTATGAATGGTCCAGCCACTTTGAACCAAATCCAGCAGAATCAATATCAAAATGGTTTCT
TGACAATGAACAACAACCAGATCATAACCAATCCTCCGCCTCCTTTGCCCTATTTGGACC
ATCATCACCAACAGCAACATCAGTCTTCTCCTCAATTTAATTACCTGATGAACAATGAAG
AACTTCTTCAAGCCTCTGGCCTCTCTGCGACAGATCTTGAACTCACTTATCCAAGTTTAC
CATATGATCCACAAGAGTATCTAATCAATGGCTACAATTATAATTAGTCATATAGCCCTT
CTCTTTACTTAAGGCAGTCTATGTATGACAAATAATATGCGACTTCCCTTGTGAGTCACA
ATATTGTTTCATTATTC
>G2430 Amino Acid Sequence (domain in AA coordinates:425-478)
MLVGKISGYEDNTRSLERETSEITSLLSQFPGNTNVLVVDTNFTTLLNMKQIMKQYAYQV
SIETDAEKALAFLTSCKHEINIVIWDFHMPGIDGLQALKSITSKLDLPVVIMSDDNQTES
VMKATFYGACDYVVKPVKEEVMANIWQHIVRKRLIFKPDVAPPVQSDPARSDRLDQVKAD
FKIVEDEPIINETPLITWTEEIQPVQSDLVQANKFDQVNGYSPIMNQDNMFNKAPPKPRM
TWTEVIQPVQSNLVQTKEFGQLNDYSQIMNQDSMYNKAATKPQLTWTEEIQPVQSGLVQA
NEFSKVNGYSQSMNQDSMFNKSATNPRLTWNELLQPVQSDLVQSNEFSQFSDYSQIMNED
NMFNKAAKKPRMTWSEVFQPVQSHLVPTDGLDRDHFDSITINGGNGIQNMEKKQGKKPRK
PRMTWTEELHQKFLEAIEIIGGIEKANPKVLVECLQEMRIEGITRSNVASHLQKHRINLE
ENQIPQQTQGNGWATAYGTLAPSLQGSDNVNTTIPSYLMNGPATLNQIQQNQYQNGFLTM
NNNQIITNPPPPLPYLDHHHQQQHQSSPQFNYLMNNEELLQASGLSATDLELTYPSLPYD
PQEYLINGYNYN*
>G2517 (66..899)
TCCTCACTCTCTCTCTTTTTCTCTAACCATAAAATCTCTTTGATCTCTTTCTCTGTGTTT
TGATAATGGAAAATGTTGGTGTTGGGATGCCGTTTTACGATTTAGGGCAAACAAGGGTTT
ACCCACTCTTGTCTGATTTCCACGATTTATCGGCGGAGAGGTATCCGGTAGGGTTCATGG
ATTTACTGGGTGTTCATCGTCATACACCCACCCATACGCCGTTGATGCATTTTCCGACCA
CACCTAACTCGTCCTCGAGCGAAGCTGTGAATGGAGATGACGAAGAAGAAGAAGATGGAG
AAGAACAGCAGCATAAGACAAAGAAGCGGTTTAAATTCACTAAAATGAGTAGAAAGCAGA
CGAAGAAGAAGGTGCCAAAAGTGTCATTCATCACGAGGAGTGAGGTTCTTCATCTAGATG
ATGGTTATAAGTGGAGAAAATACGGTCAAAAAACCTGTCAAAGACAGCCCTTTTCCAAGAA
ATTATTACCGTTGCACAACAACTTGGTGTGACGTGAAGAAGAGAGTAGAGAGATCATTCA

GTGATCCAAGCAGTGTAATCACCACTTACGAAGGTCAACATACTCATCCTCGTCCACTAC
TCATCATGCCCAAAGAAGGCAGCTCTCCATCCAATGGCTCAGCTTCTAGGGCCCACATTG
GCCTCCCTACACTCCCTCCTCAGCTTTTAGATTACAACAACCAACAACAACAAGCGCCGT
CTTCTTTTGGAACCGAGTACATTAACAGGCAAGAAAAAGGAATTAATCATGATGATGATG
ACGATCATGTTGTGAAGAAGAGTCGAACTCGGGATCTGCTGGATGGAGCTGGTTTAGTCA
AAGATCATGGCCTTCTTCAGGATGTTGTTCCCTCTCATATCATTAAGGAAGAGTATTAGT
TAATCGCATAATTATGTAGCTAGCTAGCTAG
>G2517 Amino Acid Sequence (domain in AA coordinates: TBD)
MENVGVGMPFYDLGQTRVYPLLSDFHDLSAERYPVGFMDLLGVHRHTPTHTPLMHFPTTP
NSSSSEAVNGDDEEEEDGEEQQHKTKKRFKFTKMSRKQTKKKVPKVSFITRSEVLHLDDG
YKWRKYGQKPVKDSPFPRNYYRCTTTWCDVKKRVERSFSDPSSVITTYEGQHTHPRPLLI
MPKEGSSPSNGSASRAHIGLPTLPPQLLDYNNQQQQAPSSFGTEYINRQEKGINHDDDDD
HVVKKSRTRDLLDGAGLVKDHGLLQDVVPSHIIKEEY*
>G2521 (103..768)
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TCTTTCAATACGACTGCGGAGATCAGAGCCAATTATTTGGTTATGGCGTCTCTGATCTCA
GATATTGAACCGCCGACGAGTACTACTTCAGATCTCGTTCGGAGAAAGAAGAGATCCTCT
GCTTCATCCGCCGCATCGTCTCGTTCAAGCGCATCTTCCGTCTCCGGTGAGATTCACGCG
CGATGGCGATCGGAGAAGCAACAACGGATCTACTCAGCCAAACTGTTCCAAGCGCTCCAA
CAAGTCCGCCTCAACTCTTCCGCCTCAACATCATCATCTCCAACGGCTCAGAAACGAGGA
AAGGCCGTCCGTGAAGCCGCCGATCGAGCTCTTGCCGTTTCCGCTCGGGGAAGAACACTC
TGGAGCAGAGCGATCTTAGCTAATCGGATCAAACTGAAATTTCGTAAACAGAGACGTCCT
CGAGCTACGATGGCGATTCCGGCCATGACTACGGTGGTTAGTAGCAGCAGCAACAGATCG
AGAAAACGGAGAGTGTCGGTGTTGAGATTGAATAAGAAGAGTATACCGGATGTTAACCGG
AAAGTACGTGTTCTAGGCCGGTTAGTTCCCGGTTGCGGTAAACAATCCGTACCGGTGATT
CTAGAAGAAGCAACTGATTATATTCAGGCTCTGGAGATGCAAGTGAGAGCCATGAACTCT
TTAGTTCAGCTTCTCTCCTCCTACGGCTCAGCTCCTCCACCGATTTGATGAGGTTAAAAT
CGTCTTTTTAATTCTACCATCTCTCGATCTTTCACAGCTTATGTGTATATAGAAGATTCG
GTTTGATTATAATCTGTAACTACTCTTCCCAACCGCTGATTCTTCTCTGCTACAAGTAAA
AGTAAATTTTGAACCGAGTCTTCCCATTTTTACGATCCTCAAGTCTAAATTAAGTATATG
ATTGATTAATAAAGTCTTTACCATTAGGGTTC
>G2521 Amino Acid Sequence (domain in AA coordinates: 145-213)
MASLISDIEPPTSTTSDLVRRKKRSSASSAASSRSSASSVSGEIHARWRSEKQQRIYSAK
LFQALQQVRLNSSASTSSSPTAQKRGKAVREAADRALAVSARGRTLWSRAILANRIKLKF
RKQRRPRATMAIPAMTTVVSSSSNRSRKRRVSVLRLNKKSIPDVNRKVRVLGRLVPGCGK
QSVPVILEEATDYIQALEMQVRAMNSLVQLLSSYGSAPPPI*
>G258 (60..983)
AGTGACCACCCTGCTGGTTAATCAACACCAAGAGACCTTGTAATATATAAGTTAGGAAGA
TGAGAGAGAAGTGGGAAATGAAAAGAGATGAAATGGGACATCGATGTTGTGGAAAACACA
AAGTGAAGAGAGGTCTTTGGTCTCCAGAGGAAGACGAGAAGCTTCTTCGTTATATCACCA
CTCATGGTCATCCTAGTTGGAGTTCCGTTCCAAAGCTTGCCGGGTTGCAGAGATGTGGGA
AGAGTTGCAGATTAAGGTGGATAAACTATCTAAGGCCTGATCTGAGGAGAGGTTCGTTTA
ATGAGGAAGAAGAGCAGATTATCATCGACGTACATCGTATTCTTGGTAACAAATGGGCTC
AGATTGCTAAGCACTTACCTGGACGCACTGATAATGAAGTCAAGAACTTTTGGAACTCAT
GCATTAAGAAGAAACTTCTTTCTCAAGGCTTAGATCCTTCTACACATAATCTTATGCCTT
CACACAAAAGATCTTCTTCTTCAAACAATAATAATATCCCCAAGCCAAACAAAACGACGT
CCATCATGAAGAACCCTACTGATCTTGATCAATCAACCACTGCTTTTTCAATCACAAACA
TCAATCCACCCACTTCCACTAAACCAAACAAACTTAAATCTCCTAACCAGACTACAATCC
CATCTCAAACCGTGATCCCTATCAATGATAACATGTCAAGTACTCAAACCATGATCCCTA
TCAATGATCCCATGTCAAGTCTTTTAGATGATGAGAATATGATTCCTCACTGGTCAGATG
TTGATGGAATGGCGATCCACGAAGCTCCGATGTTGCCTAGTGATAAGGCAGTAGTGGGAG
TGGATGATGATGATCTCAACATGGACATTTTGTTTAACACTCCTTCTTCTTCTGCTTTTG
ATCCTGATTTTGCTTCCATTTTCTCCTCTGCAATGTCTATCGATTTCAATCCCATGGATG
ATCTTGGCAGCTGGACCTTTTAGCTTTTACTCTACAGC
>G258 Amino Acid Sequence (domain in AA coordinates: 24-124)
MREKWEMKRDEMGHRCCGKHKVKRGLWSPEEDEKLLRYITTHGHPSWSSVPKLAGLQRCG
KSCRLRWINYLRPDLRRGSFNEEEEQIIIDVHRILGNKWAQIAKHLPGRTDNEVKNFWNS

CIKKKLLSQGLDPSTHNLMPSHKRSSSSNNNNIPKPNKTTSIMKNPTDLDQSTTAFSITN
INPPTSTKPNKLKSPNQTTIPSQTVIPINDNMSSTQTMIPINDPMSSLLDDENMIPHWSD
VDGMAIHEAPMLPSDKAVVGVDDDDLNMDILFNTPSSSAFDPDFASIFSSAMSIDFNPMD
DLGSWTF*
>G280 (108..722)
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CACACAGATTCCTTCCTTCATCACCTCACACACTCTCTACGCTTGACATGGCCTTCGATC
TCCACCATGGCTCAGCTTCAGATACGCATTCATCAGAACTTCCGTCGTTTTCTCTCCCAC
CTTATCCTCAGATGATAATGGAAGCGATTGAGTCCTTGAACGATAAGAACGGCTGCAACA
AAACGACGATTGCTAAGCACATCGAGTCGACTCAACAAACTCTACCGCCGTCACACATGA
CGCTGCTCAGCTACCATCTCAACCAGATGAAGAAAACCGGTCAGCTAATCATGGTGAAGA
ACAATTATATGAAACCAGATCCAGATGCTCCTCCTAAGCGTGGTCGTGGCCGTCCTCCGA
AGCAGAAGACTCAGGCCGAATCTGACGCCGCTGCTGCTGCTGTTGTTGCTGCCACCGTCG
TCTCTACAGATCCGCCTAGATCTCGTGGCCGTCCACCGAAGCCGAAAGATCCATCGGAGC
CTCCCCAGGAGAAGGTCATTACCGGATCTGGAAGGCCACGAGGACGACCACCGAAGAGAC
CGAGAACAGATTCGGAGACGGTTGCTGCGCCGGAACCGGCAGCTCAGGCGACAGGTGAGC
GTAGGGGACGTGGGAGACCTCCGAAGGTGAAGCCGACGGTGGTTGCTCCGGTTGGGTGCT
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>G280 Amino Acid Sequence (domain in AA coordinates: 97-104,130-137-155-162,185-192)
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>G3 (16..477)
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>G3 Amino Acid Sequence (domain in AA coordinates: 28-95)
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>G343 (1..795)
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>G343 Amino Acid Sequence (domain in AA coordinates: 178-214)
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>G363 (1..780)
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>G363 Amino Acid Sequence (domain in AA coordinates: 87-108)
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>G370 (1..774)
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>G370 Amino Acid Sequence (domain in aa coordinates: 97-117)
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>G385 (37..2202)
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>G385 Amino Acid Sequence (domain in AA coordinates: 60-123)
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>G439 (128..967)
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>G439 Amino Acid Sequence (domain in AA coordinates: 110-177)
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>G440 (237..1301)
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>G5 (417..1421)
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>G550 (1..1374)
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>G670 (28..1152)
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>G760 (175..1878)
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>G760 Amino Acid Sequence (domain in AA coordinates: 12-156)
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>G898 Amino Acid Sequence (domain in AA coordinates: 148-185)
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KSKLEIKRNEEKSPMLLIPKVETGLGLGLSSSSIRRKGIVASCGFTSNSMPQPPTPAVPQ
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>G960 (63..1538)
TACCGTCGACCCACGCGTCCGAGTGTATTCAAAGTCGGAAAGAAACCCTAAAGAAGAGGA
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AAGAGCTCGTCAATCACTACCTCCGTCTCAAGATCAACGGACGTCACTCCGATGTCCGTG
TCATCCCTGATATCGATGTCTGCAAATGGGAACCTTGGGATCTTCCTGCTCTCTCGGTGA
TTAAGACGGATGATCCAGAGTGGTTCTTTTTCTGCCCTCGTGATCGGAAATACCCTAATG
GTCATCGCTCTAACAGAGCAACTGACTCTGGCTATTGGAAAGCTACTGGTAAAGATCGTA
GCATCAAGTCTAAGAAGACTTTAATCGGTATGAAGAAGACTCTTGTCTTCTATCGTGGAC
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CTGATGATCGGGTTAATGGTGTCAAGTCCGATGAAGCAGCTTTTACGGCCAGCAACAAAT
ACTCACCTGATGATACATCATCTGATCTTGTTCAAGAAACACCTTCCTCTGATGCTGCTG
TTGAGAAACCATCAGATTATTCAGGTGGATGCGGTTATGCTCATAGTAATAGTACCGCAG
ATGGGACAATGATTGAGGCACCTGAAGAGAATCTTTGGTTATCTTGTGACCTTGAAGATC
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AGGAGGTGTTCAATAACCCTGATGACTTCTCTTGCGAGGAATCGATCAGTCGAGAGAATC
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TGCAGTATGGTTCAGAAGGTGGAGCTTCTGGTTGGCCAAGTGACACTAATTCATACTATA
GTGATTTGGTTCAGCAAGAGCAAATGATCAATCATAACACAGAGAACAACCTCACAGAAG
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ACCAGGGTATTGCTCCAAGGAGAATCCGTCTGCAGCTGCAGTCTAACTCTGAAGTAAAAG
AACGAGAGGAGGTGAATGAAGGACACACTGTTATTCCCGAGGCCAAAGAAGCTGCAGCTA
AATACTCAGAGAAGAGTGGTTCTTTGGTTAAACCTCAAATAAAGCTCAGGGCGCGGGGAA
CTATAGGCCAAGTAAAAGGAGAGAGATTTGCAGACGACGAGGTACAGGTGCAGAGCACAA
AGAGAGAGAGAGAGAGAATCAAATGTAGTTTAATGTAATTAGGGATGATGCAATGTTAGC
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AAAGAAAAAAAAAAAAAAAAAAAAAAAAAAA
>G960 Amino Acid Sequence (domain in AA coordinates: 13-156)
MGAVSMESLPLGFRFRPTDEELVNHYLRLKINGRHSDVRVIPDIDVCKWEPWDLPALSVI
KTDDPEWFFFCPRDRKYPNGHRSNRATDSGYWKATGKDRSIKSKKTLIGMKKTLVFYRGR
APKGERTNWIMHEYRPTLKDLDGTSPGQSPYVLCRLFHKPDDRVNGVKSDEAAFTASNKY
SPDDTSSDLVQETPSSDAAVEKPSDYSGGCGYAHSNSTADGTMIEAPEENLWLSCDLEDQ
KAPLPCMDSIYAGDFSYDEIGFQFQDGTSEPDVSLTELLEEVFNNPDDFSCEESISRENP
AVSPNGIFSSAKMLQSAAPEDAFFNDFMAFTDTDAEMAQLQYGSEGGASGWPSDTNSYYS
DLVQQEQMINHNTENNLTEGRGIKIRARQPQNRQSTGLINQGIAPRRIRLQLQSNSEVKE
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RERERIKCSLM*
>G991 (6..533)

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TAAAGACCTCCCACGCCTTCTCACTCTCACCTAGAAAACATGGCAAGGAATAGAGAGAGG
TTGGCCAAAATCATCAGTTCGATGGTTTGTTTTTAATGTAATTTTTGTGGAAACTAATGG
GGTTTGGCTTTGATTTACTGGTTTTCTTTTTCACTTATGTACTAGGTTTTTGCTTGCTAT
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>G991 Amino Acid Sequence (domain in AA coordinates: 7-14,48-59,82-115,128-164)
MEEEKRLELRLAPPCHQFTSNNNINGSKQKSSTKETSFLSNNRVEVAPVVGWPPVRSSRR
NLTAQLKEEMKKKESDEEKELYVKINMEGVPIGRKVNLSAYNNYQQLSHAVDQLFSKKDS
WDLNRQYTLVYEDTEGDKVLVGDVPWEMFVSTVKRLHVLKTSHAFSLSPRKHGKE*

>G748 (98..1444)
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AGCTATTAAGCTTTTCGGTATGAAAATCCCTTTTCCGTCGGTTTTTGAATCGGCAGTTAC
GGTGGAGGATGACGAAGAAGATGACTGGAGCGGCGGAGATGACAAATCACCAGAGAAGGT
AACTCCAGAGTTATCAGATAAGAACAACAACAACTGTAACGACAACAGTTTTAACAATTC
GAAACCCGAAACCTTGGACAAAGAGGAAGCGACATCAACTGATCAGATAGAGAGTAGTGA
CACGCCTGAGGATAATCAGCAGACGACACCTGATGGTAAAACCCTAAAGAAACCGACTAA
GATTCTACCGTGTCCGAGATGCAAAAGCATGGAGACCAAGTTCTGTTATTACAACAACTA
CAACATAAACCAGCCTCGTCATTTCTGCAAGGCTTGTCAGAGATATTGGACTGCTGGAGG
GACTATGAGGAATGTTCCTGTGGGGGCAGGACGTCGTAAGAACAAAAGCTCATCTTCTCA
TTACCGTCACATCACTATTTCCGAGGCTCTTGAGGCTGCGAGGCTTGACCCGGGCTTACA
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CATGACACCTGTTATGAAGCTACAAGAAGATCAAAAGGTCTCAAACGGTGCTAGGAACAG
GTTTCACGGGTTAGCGGATCAACGGCTTGTAGCTCGGGTAGAGAATGGAGATGATTGCTC
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CGGCAGTGTTGTTGAAGCACAAATGAACAACAACAACAACAATAACATGAATGGTTATGC
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TTACCCGCCTCCAGGGTATCCAATGCCGTTTTACCCTTACTGGACCATCCCAATGCTACC
ACCGCATCAATCCTCATCGCCTATAAGCCAAAAGTGTTCAAATACAAACTCTCCGACTCT
CGGAAAGCATCCGAGAGATGAAGGATCATCGAAAAAGGACAATGAGACAGAGCGAAAACA
GAAGGCCGGGTGCGTTCTGGTCCCGAAAACGTTGAGAATAGATGATCCTAACGAAGCAGC
AAAGAGCTCGATATGGACAACATTGGGAATCAAGAACGAGGCGATGTGCAAAGCCGGTGG
TATGTTCAAAGGGTTTGATCATAAGACAAAGATGTATAACAACGACAAAGCTGAGAACTC
CCCTGTTCTTTCTGCTAACCCTGCTGCTCTATCAAGATCACACAATTTCCATGAACAGAT
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TTTACATGTTTTGGTTCTCTGTACACTATTTGATTTACCTTTTTTACTTTCTTTCTTCAT
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GTTGGCATTTCAAAAAAAAAAAAAAAAA

>G748 Amino Acid Sequence (domain in AA coordinates: 112-140)
MMMETRDPAIKLFGMKIPFPSVFESAVTVEDDEEDDWSGGDDKSPEKVTPELSDKNNNNC
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KFCYYNNYNINQPRHFCKACQRYWTAGGTMRNVPVGAGRRKNKSSSSHYRHITISEALEA
ARLDPGLQANTRVLSFGLEAQQQHVAAPMTPVMKLQEDQKVSNGARNRFHGLADQRLVAR
VENGDDCSSGSSVTTSNNHSVDESRAQSGSVVEAQMNNNNNNNMNGYACIPGVPWPYTWN
PAMPPPGFYPPPGYPMPFYPYWTIPMLPPHQSSSPISQKCSNTNSPTLGKHPRDEGSSKK
DNETERKQKAGCVLVPKTLRIDDPNEAAKSSIWTTLGIKNEAMCKAGGMFKGFDHKTKMY
NNDKAENSPVLSANPAALSRSHNFHEQI*

>G247 (1..660)
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CTCCACAAGCTCCTCGGCAACAGATGGTCGTTGATAGCGAAAAGAGTTCCGGGAAGAACA
GACAACCAAGTAAAGAATTACTGGAACACACATCTCAGCAAGAAACTTGGTCTCGGAGAT
CATTCAACTGCCGTCAAAGCCGCATGCGGTGTAGAGTCTCCACCGTCTATGGCCCTTATA
ACCACAACGTCCTCCTCTCATCAAGAGATCTCCGGTGGAAAAAATTCAACTCTAAGGTTC
GACACTTTAGTTGACGAATCCAAACTCAAACCAAAATCCAAACTAGTCCACGCAACACCA
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>G247 Amino Acid Sequence (domain in AA coordinates: 15-116)
MRMTRDGKEHEYKKGLWTVEEDKILMDYVRTHGQGHWNRIAKKTGLKRCGKSCRLRWMNY
LSPNVNRGNFTDQEEDLIIRLHKLLGNRWSLIAKRVPGRTDNQVKNYWNTHLSKKLGLGD
HSTAVKAACGVESPPSMALITTTSSSHQEISGGKNSTLRFDTLVDESKLKPKSKLVHATP
TDVEVAATVPNLFDTFWVLEDDFELSSLTMMDFTNGYCL*
>G585 (111..2039)
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AAACAATGGCTACCGGACAAAACAGAACAACTGTGCCAGAGAATCTGAAGAAACACCTCG
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CTCAAGTCACCAGACGAGCTTCCGCCGCCGCACTTTCACCGGAAGATCTCGCCGACACCG
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CGGCTGGACGGGTTGCTTACGGTGCAAGAAAGAGTAGAGTTCAAAGACTAGGGCAAATTC
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TTTTTTGTGTCTTTTTTTCCGTTGCTTAACGTAGGTGAAGAGGAACATACACTATGCGTA
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TTTGTGTTCTTTTGTTGTT

>G585 Amino Acid Sequence (domain in AA coordinates:436-501)
MDEETMATGQNRTTVPENLKKHLAVSVRNIQWSYGIFWSVSASQSGVLEWGDGYYNGDIK
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ADTEWYYLVCMSFVFNIGEGMPGRTFANGEPIWLCNAHTADSKVFSRSLLAKSAAVKTVV
CFPFLGGVVEIGTTEHITEDMNVIQCVKTSFLEAPDPYATILPARSDYHIDNVLDPQQIL
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DVHYQSVISTIFKTNHQLILGPQFRNCDKQSSFTRWKKSSSSSSGTATVTAPSQGMLKKI
IFDVPRVHQKEKLMLDSPEARDETGNHAVLEKKRREKLNERFMTLRKIIPSINKIDKVSI
LDDTIEYLQELERRVQELESCRESTDTETRGTMTMKRKKPCDAGERTSANCANNETGNGK
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HSVQSSTGDGLLCLTVNCKHKGSKIATPGMIKEALQRVAWIC*
>G634 (1..798)
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GGTGGATTAGGAGGTGGAGGTGGAGGAGGAGGAGGAGGAAGTGCTTCTTCTTCATCGGGA
AATCGATGGCCGAGAGAAGAAACTTTAGCTCTTCTTCGGATCCGATCCGATATGGATTCT
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CTGAGAAGTGGAATGGAACCAAGGTACCAAGATAATGTACCTAAAGGACTTCTATGGGAA
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AACAACAAGAATCAATGA
>G634 Amino Acid Sequence (domain in aa coordinates: 62-147, 189-245)
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KWENINKYYKKVKESNNSNYNNKNQ*
>G676 (1..612)
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cactgtttttga
>G676 Amino Acid Sequence (domain in AA coordinates: 17-119)
MRKKVSSSGDEGNNEYKKGLWTVEEDKILMDYVKAHGKGHWNRIAKKTGLKRCGKSCRLR
WMNYLSPNVKRGNFTEQEEDLIIRLHKLLGNRWSLIAKRVPGRTDNQVKNYWNTHLSKKL
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VHEDEFELSTLTNMMDFIDGHCF*
>G682 (1..228)
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>G682 Amino Acid Sequence (domain in AA coordinates 27-63)
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GRTAGEIERFWVMKN*
>G635 (1..993)
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GAAGTCCTGAGGAAGATTGTAAGGAAGTACAGTGGTAAAAGGCCTGAAGTCATCGCTATA
GCCACTGAGAATCCAATGGCTGTCCGAGCTGATGAGGTCAGTGCGAGACTGTCTGGTGAT
CCAAGTGTTGGTTCTGGAGTTGCAGCTTTAAGGAAAGTTGTTGAAGGAAATGACAAAAGA
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>G635 Amino Acid Sequence (domain in AA coordinates: 239-323)
MEIMRPGVSENTLKGKIRITTRCMWLDKGRLLDALHKAAHAALSSCPVTCPLSHMERTVS
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SRAKKAPSQEASPKEVDRTLEDDIIDSARLLAEEETAASTYTEEVDTPVGSSSEESDDFW
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ESKADERSKTSWPHFEDMNNILSELGTPAS*
>G1068 (150..1310)
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AAGACTTGTTCTTTTTCTCCTATATTCAACGAATTATCCACTTTAA
>G1068 Amino Acid Sequence (domain in AA coordinates: 143-150)
MDSREIHHQQQQQQQQQQQQQQQQHLQQQQPPPGMLMSHHNSYNRNPNAAAAVLMGHN
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GNEGGGGGDSAGANANSSDPPAKRNRGRPPGSGKKQLDALGGTGGVGFTPHVIEVKTGED
IATKILAFTNQGPRAICILSATGAVTNVMLRQANNSNPTGTVKYEGRFEIISLSGSFLNS
ESNGTVTKTGNLSVSLAGHEGRIVGGCVDGMLVAGSQVQVIVGSFVPDGRKQKQSAGRAQ
NTPEPASAPANMLSFGGVGGPGSPRSQGQQHSSESSEENESNSPLHRRSNNNNSNNHGIF
GNSTPQPLHQIPMQMYQNLWPGNSPQ*
>G1225 (1..984)
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>G1225 Amino Acid Sequence (domain in AA coordinates: 78-147)
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>G1337 Amino Acid Sequence (domain in AA coordinates: 9-75)
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>G1759 (110..700)
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>G1804 Amino Acid Sequence (domain in AA coordinates: 357-407)
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>G207 Amino Acid Sequence (domain in AA coordinates: 6-106)
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PKVE*
>G218 (1..1182)
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>G218 Amino Acid Sequence (domain in AA coordinates: TBD)
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>G241 (46..867)
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>G241 Amino Acid Sequence (domain in AA coordinates: 14-114)
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>G254 Amino Acid Sequence (domain in AA coordinates: 62-106)
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>G26 Amino Acid Sequence (domain in AA coordinates: 67-134)
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>G263 (48..902)
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>G263 Amino Acid Sequence (domain in AA coordinates: TBD)
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>G308 (196..1794)
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GAAAAAAACCCAACCATGAAGAGAGATCATCATCATCATCATCAAGATAAGAAGACTATG
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AAGGTTAGGTCATCGGAAATGGCTGATGTTGCTCAGAAACTCGAGCAGCTTGAAGTTATG
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GTTGTCCTGGTTGACTCGCAGGAGAACGGTGTGCGTCTCGTTCACGCGCTTTTGGCTTGC
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CTCGCGCGGCGGATTTACCGTCTCTCTCCGTCGCAGAGTCCAATCGACCACTCTCTCTCC
GATACTCTTCAGATGCACTTCTACGAGACTTGTCCTTATCTCAAGTTCGCTCACTTCACG
GCGAATCAAGCGATTCTCGAAGCTTTTCAAGGGAAGAAAAGAGTTCATGTCATTGATTTC
TCTATGAGTCAAGGTCTTCAATGGCCGGCGCTTATGCAGGCTCTTGCGCTTCGACCTGGT
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>G308 Amino Acid Sequence (domain in AA coordinates: 270-274)
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STLFDSLEGVPSGQDKVMSEVYLGKQICNVVACDGPDRVERHETLSQWRNRFGSAGFAAA
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>G38 (149..1156)
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TGCTGAGATCAGAGAGCCTAATCGAGGTAGCAGGCTTTGGCTTGGTACTTTCCCTACTGC
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CCACAACGACTGTTGATTCTCTATCCGAGTTTTAGTGATATAGAGAACTACAGAACACGT
TTTTTCTTGTTATAAAGGTGAACTGTATATATCGAAACAGTGATATGACAATAGAGAAGA
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TAACAACAGGAATGAATAATACACACTTGTGAAGCTTTTAAAAAAAAAAAAAAAAAAAAA
>G38 Amino Acid Sequence (domain in AA coordinates: 76-143)
MAVYDQSGDRNRTQIDTSRKRKSRSRGDGTTVAERLKRWKEYNETVEEVSTKKRKVPAKG
SKKGCMKGKGGPENSRCSFRGVRQRIWGKWVAEIREPNRGSRLWLGTFPTAQEAASAYDE
AAKAMYGPLARLNFPRSDASEVTSTSSQSEVCTVETPGCVHVKTEDPDCESKPFSGGVEP
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FDPLQSLNYGIPPFQLEGKDGNGFFDDLSYLDLEN*
>G43 (38..643)
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AAAAAAAAA
>G43 Amino Acid Sequence (domain in AA coordinates: 104-172)
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RRTDVPQPQGTTTSTSSSSSN*
>G536 (1..768)
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>G536 Amino Acid Sequence (domain in AA coordinates:226-233)
MSTREENVYMAKLAEQAERYEEMVEFMEKVAKTVDVEELSVEERNLLSVAYKNVIGARRA
SWRIISSIEQKEESKGNEDHVAIIKDYRGEIESELSKICDGILNVLEAHLIPSASPAESK
VFYLKMKGDYHRYLAEFKAGAERKEAAESTLVAYKSASDIATAELAPTHPIRLGLALNFS
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AGDEIKEASKPDGAE*
>G567 (38..1273)
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>G567 Amino Acid Sequence (domain in AA cordinates 210-270)
MNSIFSIDDFSDPFWETPPIPLNPDSSKPVTADEVSQSQPEWTFEMFLEEISSSAVSSEP
LGNNNNAIVGVSSAQSLPSVSGQNDFEDDSRFRDRDSGNLDCAAPMTTKTVNVDSDDYRR
VLKNKLEAECATGVSLRVGSVKPEDSTSSPETQLQPVQSSPLTQGELGVTSSLPAEVKKT
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SDLETQVNDLKGEHSSLLKQLSNMNHKYDEAAVGNRILKADIETLRAKVKMAEETVKRVT
GMNPMLLGRSSGHNNNNRMPITGNNRMDSSSIIPAYQPHSNLNHMSNQNIGIPTILPPRL
GNNFAAPPSQTSSPLQRIRNGQNHHVTPSANPYGWNTEPQNDSAWPKKCVD*
>G680 (338..2275)
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TTTGCTTCTCCAATCTTTATGAAAGAGACTTTTAATTTTCCTTCCGAACATTTCTTTGGT
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>G680 Amino Acid Sequence (domain in AA coordinates: 24-70)
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SHGLLPVCAPAPITCVPFSTVAVPTPAMTEMDTVENTQPFEKQNTALQDQTLASKSPASS
SDDSDETGVTKLNADSKTNDDKIEEVVVTAAVHDSNTAQKKNLVDRSSCGSNTPSGSDAE
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ALFARERLPQSFSPPQVAENVNRKQSDTSMPLAPNFKSQDSCAADQEGVVMIGVGTCKSL
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>G867 (64..1098)
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>G867 Amino Acid Sequence (domain in AA coordinates: 59-124)
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>G956 (1..840)
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>G956 Amino Acid Sequence (domain in AA coordinates: TBD)
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LRTLLSQLTKKVEESQSRGDGSSESQLTDIGIPSHAWNY*
>G996 (53..1063)
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>G996 Amino Acid Sequence (domain in AA coordinates: 14-114)
MGRHSCCYKQKLRKGLWSPEEDEKLLRYITKYGHGCWSSVPKQAGLQRCGKSCRLRWINY
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>G778 Amino Acid Sequence (domain in AA coordinates: 220-267)
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>G791 (173..877)
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>G861 (158..880)
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>G861 Amino Acid Sequence (domain in AA coordinates: 2-57)
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>G938 (1..1755)
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>G938 Amino Acid Sequence (domain in AA coordinates: 96-104)
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>G965 (73..1956)
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ATC

>G965 Amino Acid Sequence (domain in AA coordinates: 423-486)
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>G1143 (54..677)
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>G1143 Amino Acid Sequence (domain in AA coordinates:33-82)
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>G1190 (209..2020)
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>G1198 (230..1675)
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F*
>G1226 (212..1159)
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>G1496 Amino Acid Sequence (domain in AA coordinates: 184-248)
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>G1526 Amino Acid Sequence (domain in AA coordinates: 493-620, 864-1006)
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>G1640 Amino Acid Sequence (domain in AA coordinates: 14-115)
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>G1644 (1..348)
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>G1644 Amino Acid Sequence (conserved domain in AA coordinates:39-102)
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>G1646 (34..786)
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>G1646 Amino Acid Sequence (domain in AA coordinates: 72-162)
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WLHAEENKRRTLQKNDIAAAITRTDIFDFLVDIVPREEIKEEEDAASALGGGGMVAPAAS
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SGHGNLDSQG*
>G1672 (239..1399)
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CCTCGTACCG
>G1672 Amino Acid Sequence (conserved domain in AA coordinates: 41-194)
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>G1677 (24..1037)
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>G1677 Amino Acid Sequence (conserved domain in AA coordinates:17-181)
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>G1765 (139..966)
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>G1765 Amino Acid Sequence (conserved domain in AA coordinates: 20-140)
MSGEGNLGKDHEEENEAPLPGFRFHPTDEELLGYYLRRKVENKTIKLELIKQIDIYKYDP
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>G1777 (97..1878)
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>G1777 Amino Acid Sequence (domain in AA coordinates:124-247)
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>G1793 (59..1783)
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>G1793 Amino Acid Sequence (conserved domain in AA coordinates:179-255, 281-349)
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>G180 (54..629)
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>G180 Amino Acid Sequence (domain in AA coordinates: 118-174)
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>G192 (63..959)
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>G192 Amino Acid Sequence (domain in AA coordinates: 128-185)

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>G1948 (18..1118)
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>G1948 Amino Acid Sequence (domain in AA coordinates: entire protein)
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>G2123 Amino Acid Sequence (domain in AA coordinates:99-109)
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>G2139 Amino Acid Sequence (conserved domain in AA coordinates:14-69)
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>G425 Amino Acid Sequence (domain in AA coordinates: TBD)
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>G1793 (59..1783)
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>G1056 Amino Acid Sequence (domain in AA coordinates 183-246)
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>G323 (77..826)
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>G323 Amino Acid Sequence (conserved domain in AA coordinates:48-96)
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CVVLCLLLF*
>G176 (41..1606)

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>G176 Amino Acid Sequence (domain in AA coordinates: 117-173,234-290)
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>G174 (194..1585)
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>G174 Amino Acid Sequence (domain in AA coordinates: TBD)
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>G715 (1..705)
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>G715 Amino Acid Sequence (domain in AA coordinates: 60-132)
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>G588 (196..1599)
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>G588 Amino Acid Sequence (domain in AA coordinates: 309-376)
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>G1758 (69..677)
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>G1758 Amino Acid Sequence (domain in AA coordinates: TBD)
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>G2148 Amino Acid Sequence (conserved domain in AA coordinates:130-268)
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>G2379 (52..798)
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>G2379 Amino Acid Sequence (domain in AA coordinates:19-110, 173-232)
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>G1462 (63..1031)
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>G1462 Amino Acid Sequence (domain in AA coordinates: TBD)
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>G1211 (44..1120)
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>G1211 Amino Acid Sequence (domain in AA coordinates: 123-179)
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>G1048 (5..892)
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>G1048 Amino Acid Sequence (domain in AA coordinates 138-190)
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>G986 (31..846)
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TG
>G986 Amino Acid Sequence (domain in AA coordinates: 146-203)
MDYDPNTNPFDLHFSGKLPKREVSASASKVVEKKWLVKDEKRNMLQDEINRVNSENKKLT
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QQMASSLTKDPKFTAALATAISGRLIEHSRT*
>G789 (259..1593)
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>G789 Amino Acid Sequence (domain in AA coordinates: 253-313)
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>G2085 (1..930)
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>G2085 Amino Acid Sequence (domain in AA coordinates: TBD)
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DNSNLLGDH*
>G1783 (1..603)
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>G1783 Amino Acid Sequence (domain in AA coordinates: 81..129)
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IPSNQYYPSQENFRGFDQRW*
>G2072 (155..793)
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AAAAAAAAAAAAAAAAAA
>G2072 Amino Acid Sequence (conserved domain in AA coordinates:90-149)
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>G931 (85..1071)
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>G931 Amino Acid Sequence (domain in AA coordinates: TBD)
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>G278 (93..1874)
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AAAA

>G278 Amino Acid Sequence (domain in AA coordinates: 2-593)
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FAVAYCNVKTATDLLKLDLADVNHRNPRGYTVLHVAAMRKEPQLILSLLEKGASASEATL
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>G2421 (1..630)
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>G2421 Amino Acid Sequence (domain in AA coordinates: 9-110)
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AAATEKEGTLAFDVEQLWNLFDGETVIFD*

>G2032 (53..1789)
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>G958 Amino Acid Sequence (conserved domain in AA coordinates:7-156)
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GSRTDWVMHEYRLEEQECDSKSGIQDAYALCRVFKKSALANKIEEQHHGTKKNKGTTNSE
QSTSSTCLYSDGMYENLENSGYPVSPETGGLTQLGNNSSSDMETIENKWSQFMSHDTSFN
FPPQSQYGTISYPPSKVDIALECARLQNRMLPPVPPLYVEGLTHNEYFGNNVANDTDEML
SKIIALAQASHEPRNSLDSWDGGSASGNFHGDFNYSGEKVSCLEANVEAVDMQEHHVNFK
EERLVENLRWVGVSSKELEKSFVEEHSTVIPIEDIWRYHNDNQEQEHHDQDGMDVNNNNG
DVDDAFTLEFSENEHNENLLDKNDHETTSSSCFEVVKKVEVSHGLFVTTRQVTNTFFQQI
VPSQTVIVYINPTDGNECCHSMTSKEEVHVRKKINPRINGVSSTVLGQWRKFAHVIGFIP
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>G1037 (1..1722)
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CCAAAGTATGTGATGAAGGGAGTTACTCATGGTGCTTGTGATTATCTACTGAAGCCGGTT
CGTATTGAGGAGTTGAAGAACATATGGCAACATGTCGTGAGAAGTAGATTTGATAAGAAC
CGTGGGAGTAATAATAATGGTGATAAGAGAGATGGATCAGGTAATGAAGGTGTTGGGAAT
TCTGATCCGAACAATGGGAAAGGTAATAGAAAACGTAAAGATCAGTATAATGAAGATGAG
GATGAGGATAGAGATGATAATGATGATTCGTGTGCTCAAAAGAAGCAACGTGTTGTTTGG
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CATGTCTCATCACTTCCTCTTAACCACAGTGATGGAGGAAACATACTTCAAGGGTTGCCA
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CCAGGCTTCCCAGGACACCAGATCAATAAACGTTTGGAGCATTGGTCAAATGCTGTATCC
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>G1037 Amino Acid Sequence (domain in AA coordinates: 11-134, 200-248)
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RIEELKNIWQHVVRSRFDKNRGSNNNGDKRDGSGNEGVGNSDPNNGKGNRKRKDQYNEDE
DEDRDDNDDSCAQKKQRVVWTVELHKKFVAAVNQLGYEKAMPKKILDLMNVEKLTRENVA

SHLQKFRLYLKRISGVANQQAIMANSELHFMQMNGLDGFHHRPIPVGSGQYHGGAPAMRS
FPPNGILGRLNSSSGIGVRSLSSPPAGMFLQNQTDIGKFHHVSSLPLNHSDGGNILQGLP
MPLEFDQLQTNNNKSRNMNSNKSIAGTSMAFPSFSTQQNSLISAPNNNVVVLEGHPQATP
PGFPGHQINKRLEHWSNAVSSSTHPPPPAHNSNSINHQFDVSPLPHSRPDPLEWNNVSSS
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GFVVGQQKLQSGGFMVADAGSLDDIVNSTMKQV*
>G2065 (33..1124)
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>G2065 Amino Acid Sequence (domain in AA coordinates: TBD)
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VEGKMSQYRYDAKDLQDLLSCMNLYLDQLNGRIESIKENGESLLSSVSPFPTRIGVDEIG
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NNL*
>G2137 (77..1123)
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CGTGGCTCCAGGATGTCCCGTTAGAAAACAGGTGCAAAGGTGTTTAGAAGACATGTCAAT
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TCACGTTTCATCTTCTCAAAACCGATTAAATTGGATGATGTAGAGTTTCCTATATCTCTA
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GTTTCTAACATTTATGTTTCGTATA

>G2137 Amino Acid Sequence (conserved domain in AA coordinates:109-168)
MGIDLSLKLEAEEKKKEIEGSKHSRENKEDEEHDASGDEDEQMVKEDEDDSSSLGLRTRE
EENEREELLQLQIQMESVKEENTRLRKLVEQTLEDYRHLEMKFPVIDKTKKMDLEMFLGV
QGKRCVDITSKARKRGAERSPSMEREIGLSLSLEKKQKQEESKEAVQSHHQRYNSSSLDM
NMPRIISSSQGNRKARVSVRARCETATMNDGCQWRKYGQKTAKGNPCPRAYYRCTVAPGC
PVRKQVQRCLEDMSILITTYEGTHNHPLPVGATAMASTASTSPFLLLDSSDNLSHPSYYQ
TPQAIDSSLITYPQNSSYNNRTIRSLNFDGPSRGDHVSSSQNRLNWMM*
>G746 (1..1311)
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CCTGAGAGATCTTCTGAAGCTGTGACAAGGATCAGGACTCGGCATAGGACACGGTTCAGA
CAGCTTAATCTCCCGATCCCGGTTCTATCTGAAACCCATACCATGGCTATAGAGCTCAAC
CAGTTGATGGGAAATTCTGTAAATAGAGCTGCTATGCAGACTGGTGAGGGTAGTGAAAGA
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>G746 Amino Acid Sequence (domain in AA coordinates: 139-178)
MGEELADTMNLDLNLGPGPESDLQPAPNETVNLADWTNDPPERSSEAVTRIRTRHRTRFR
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DKKADVEKSSGSDGNFFDCNICLDLSKEPVLTCCGHLYCWPCLYQWLQISDAKECPVCKG
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QNRFDRDSTPVPDFSNREASERVNDRANSILNRLMTSRGVRSEQNQASAAAAAIVAASED
IDLNPNIAPDLEGESNTRFHPLLIRRQLQSHRVARISTFTSALSSAERLVDAYFRTHPLG
RNHQEQNHHAPVVVDDRDSFSSIAAVINSESQVDTAVEIDSMALSTSSSRRRNENGSRVS
DVDSADSRPPRRRRFT*
>G2701 (46..837)
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CACAGCTCGAGTAGCGGTAGCTGGACTAAAGAAGAGAACAAGATGTTCGAACGAGCTCTT
GCGATATACGCTGAAGACTCGCCTGATCGCTGGTTTAAAGTTGCTTCCATGATCCCTGGA
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GAAGCAGGACGTGTTCCCATTCCTGGTTATCCTGCAGCTTCTTCTCCCTTGGGGTTTGAC
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CCAAGTATCCATGACATCACAACCGGCAATCTTCTCAATGCCAATCTCAACCGTTCCTTT
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>G2701 Amino Acid Sequence (domain in AA coordinates: 33-81, 129-183)
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>G1819 (1..639)
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>G1819 Amino Acid Sequence (domain in AA coordinates: 46-188)
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DTLTRSDISAATTRSFKFTFLGDVVPRDPSVVTDDPVLHPDGEVLPPGTVIGYPVFDCNG
VYASPPQMQEWPAVPGDGEEAAGEIGGSSGGN*
>G1227 (372..1451)
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GATGC
>G1227 Amino Acid Sequence (domain in AA coordinates: 183-244)
MERSIQGQNKLCCLDQKVNVRRSLQVQETVEDHQSFALEEEEQQLSTPSLLQDTTIPFLQ
MLQQSEDPSPFLSFKDPSFLALLSLQTLEKPWELENYLPHEVPEFHSPIHSETNHYYHNP
SLEGVNEAISNQELPFNPLENARSRRKRKNNNLASLMTREKRKRRRTKPTKNIEEIESQR
MTHIAVERNRRRQMNVHLNSLRSIIPSSYIQRGDQASIVGGAIDFVKILEQQLQSLEAQK
RSQQSDDNKEQIPEDNSLRNISSNKLRASNKEEQSSKLKIEATVIESHVNLKIQCTRKQG
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>G2417 (118..1311)
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GCAAATTCTATGAAGAATTATCCGTTAAATGATGATGATGCAAATTCTATGGAGAATTAT
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>G2417 Amino Acid Sequence (domain in AA coordinates: 235-285)
MIPNDDDDANSMKNYPLNDDDANSMKNYPLNDDDANSMENYPLRSIPTELSHTCSLIPPS
LPNPSEAAADMSFNSELNQIMARPCDMLPANGGAVGHNPFLEPGFNCPETTDWIPSPLPH
IYFPSGSPNLIMEDGVIDEIHKQSDLPLWYDDLITTDEDPLMSSILGDLLLDTNFNSASK
VQQPSMQSQIQQPQAVLQQPSSCVELRPLDRTVSSNSNNNSNSNNAAAAAKGRMRWTPEL
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LTPLEQITSDDTKRGIDITETLRIQMEHQKKLHEQLESLRTMQLRIEEQGKALLMMIEKQ
NMGFGGPEQGEKTSAKTPENGSEESESPRPKRPRNEE*
>G2116 (104..1117)
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>G2116 Amino Acid Sequence (conserved domain in AA coordinates:150-210)
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GCAMYAGDIMDAKKAMPPEKLSELWNIDPKRAKRILANRQSAARSKERKARYIQELERKV
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METGEISGNSDSFDMGMQQIQYSSSTFMAIPPYHGSMNLHDMQMHSSFNPMEMSNSQSVS
DFLQNGRMQGLEISSNSSSLVKSEGPSLSASESSSAY*
>G647 (1..948)
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GATCTTGGATTCTTCTCAGGATTAGCTACTTCTCCGACTTCGATTCTTGTTTCTCCTTCG
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GTTAGGTTACCTTTTTCGTCGTCTCTGCGTCCGATTCAGGCGGCAACGTGGCCGAGGATA
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>G647 Amino Acid Sequence (domain in aa coordinates: 77-192)
MMIGENKNRPHPTIHIPQWDQINDPTATISSPFSSVNLNSVNDYPHSPSPYLDSFASLFR
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RAEMYARLSRENSLG*
>G974 (377..1162)
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>G974 Amino Acid Sequence (domain in AA coordinates: 81-140)
MTTSMDFYSNKTFQQSDPFGGELMEALLPFIKSPSNDSSAFAFSLPAPISYGSDLHSFSH
HLSPKPVSMKQTGTSAAKPTKLYRGVRQRHWGKWVAEIRLPRNRTRLWLGTFDTAEEAAL
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SRKRSSTVAVKLPEEDYSSAGSSPLLTESYGSGGSSSPLSELTFGDTEEEIQPPWNENAL
EKYPSYEIDWDSILQCSSLVN*
>G1419 (27..692)
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>G1419 Amino Acid Sequence (domain in AA coordinates: 69-137)
MASSHQQQQEQDQSALDLITQHLLTDFPSLDTFASTIHHCTTSTLSQRKPPLATIAVPTT
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>G1634 (22..855)
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GAGGGAGTTATGTTTCTTGGTCAGAATCTATCCTCGGTCTTCTCTTCCTACGATCCTGCC
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>G1634 Amino Acid Sequence (domain in AA coordinates: 129-180)
METLHPLLSHVPTSDHRFVVQEMMCLQSSSWTKEENKKFERALAVYADDTPDRWFKVAAM
IPGKTISDVMRQYSKLEEDLFDIEAGLVPIPGYRSVTPCGFDQVVSPRDFDAYRKLPNGA
RGFDQDRRKGVPWTEEEHRRFLLGLLKYGKGDWRNISRNFVGSKTPTQVASHAQKYYQRQ
LSGAKDKRRPSIHDITTVNLLNANLSRPSSDHGCLVSKQAEPKLGFTDRDNAEEGVMFLG
QNLSSVFSSYDPAIKFSGANVYGEGGYCISQDLETRK*
>G1637 (1..954)
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GCCGTTGATGATACCGGTTATCATTCCGATGGTCAGATTCATTCCAAGAAGGGTAAAACT
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CATCCTTCTGGTATACCTGTTCCAAGACATATACCGATTGGTTTGCCTCTGTCTCAACCG
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CAAGCTACTGGAGCTTCTGACTTGACTGGTCATGGCGTTATTCATGTGAAATGA
>G1637 Amino Acid Sequence (domain in AA coordinates: 109-173)
MVKETVTVAKTCSHCGHNGHNARTCLNGVNKASVKLFGVNISSDPIRPPEVTALRKSLSL
GNLDALLANDESNGSGDPIAAVDDTGYHSDGQIHSKKGKTAHEKKKGKPWTEEEHRNFLI
GLNKLGKGDWRGIAKSFVSTRTPTQVASHAQKYFIRLNVNDKRKRRASLFDISLEDQKEK
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QATGASDLTGHGVIHVK*
>G1818 (601..1161)
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>G1818 Amino Acid Sequence (domain in AA coordinates: 36-113)
MENNNNNHQQPPKDNEQLKSFWSKGMEGDLNVKNHEFPISRIKRIMKFDPDVSMIAAEAP
NLLSKACEMFVMDLTMRSWLHAQESNRLTIRKSDVDAVVSQTVIFDFLRDDVPKDEGEPV
VAAADPVDDVADHVAVPDLNNEELPPGTVIGTPVCYGLGIHAPHPQMPGAWTEEDATGAN
GGNGGN*
>G1820 (1..609)
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TTCGCAAAGGCTTGCGAAATGTTCATCGTTGATCTCACGATGCGGTCGTGGCTCAAAGCC
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CCTGGCTTTGTGGCTATGCCACATCCTGACGGTGGAGGAGTACCGCAATATTATTATCCA
CCGGGAGTGGTGATGGGAACTCCTATGGTTGGTAGTGGAATGTACGCGCCATCGCAGGCG
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GGAAATTGA
>G1820 Amino Acid Sequence (domain in AA coordinates: 70-133)
MAENNNNNGDNMNNDNHQQPPSYSQLPPMASSNPQLRNYWIEQMETVSDFKNRQLPLARI
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WPAAAGDGEDDAEDNGGNGGGN*
>G1903 (1..1200)
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>G1903 Amino Acid Sequence (domain in AA coordinates: 134-180)
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FDTKGNSNRSSLVSETSHSLQANPAAMSRAMNFRESMQQ*
>G371 (1..582)
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CAATACGATCATAAGAGGGAACCACCAAAATGTCCGGTATGCAAATCTGATGTCTCCGAG
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>G371 Amino Acid Sequence (domain in aa coordinates: 21-74)
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FLLCFMFMCLFLF*
>G597 (255..1310)
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>G597 Amino Acid Sequence (domain in AA coordinates: 97-104,137-144)
MSGSETGLMAATRESMQFTMALHQQQQHSQAQPQQSQNRPLSFGGDDGTALYKQPMRSVS
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APSFTVSQPSSGGDGGEKKRGRPPGSSSKRLKLQALGSTGIGFTPHVLTVLAGEDVSSKI
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RTGGLSVSLSSPDGNVLGGSVAGLLIAASPVQIVVGSFLPDGEKEPKQHVGQMGLSSPVL
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>G1009 (28..1704)
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>G1009 Amino Acid Sequence (domain in aa coordinates: 201-277, 303-371)
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LAVSEASPTPKKNVESFGQRTSIYRGVTRHRWTGRYEAHLWDNSCRREGQSRKGRQVYLG
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NFDISRYDVKSIASCNLPVGGLMPKPSPATAAADKTVDLSPSDSPSLTTPSLTFNVATPV
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QTAKSNLSVLHTPVFGLE*
>G170 (1..1107)
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AAGAAGATGATGGATCAAGAGACTTACCTTATGGAGAGGATTACCAAAGCAAAAGAGCAA
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>G170 Amino Acid Sequence (domain in aa coordinates: 2-57)
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NQQQSFMNPMVEQHMNHVGGRESIPFVDGNCYNYHQLPSNQLPAVDHASTSYMPSTTGVY
DPYINNNL*
>G1768 (185..1426)
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CCAAGAATGTAATGCAAAAGACAGAACTGGAAGTAATAGATAGTTTTGTCTCATAACCAT
TAATAAGGTTGAATCAAATCATATACATCCCCATGCTACAACTATTACACAGGCTCCATC
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GGAAGTGGTTACAT

>G1768 Amino Acid Sequence (domain in AA coordinates: 54-413)
MDNVRGSIMLQPLPEIAESIDDAICHELSMWPDDAKDLLLIVEAISRGDLKLVLVACAKA
VSENNLLMARWCMGELRGMVSISGEPIQRLGAYMLEGLVARLAASGSSIYKSLQSREPES
YEFLSYVYVLHEVCPYFKFGYMSANGAIAEAMKDEERIHIIDFQIGQGSQWIALIQAFAA
RPGGAPNIRITGVGDGSVLVTVKKRLEKLAKKFDVPFRFNAVSRPSCEVEVENLDVRDGE
ALGVNFAYMLHHLPDESVSMENHRDRLLRMVKSLSPKVVTLVEQECNTNTSPFLPRFLET
LSYYTAMFESIDVMLPRNHKERINIEQHCMARDVVNIIACEGAERIERHELLGKWKSRFS
MAGFEPYPLSSIISATIRALLRDYSNGYAIEERDGALYLGWMDRILVSSCAWK*

>G185 (77..988)
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CTATAGATGCACGTATAGAAAGTCTCAAGGATGTGAAGCCACTAAACAAGTCCAAAGATC
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AAAAA

>G185 Amino Acid Sequence (domain in AA coordinates: 113-172)
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YGQKDILGAKFPRGYYRCTYRKSQGCEATKQVQRSDENQMLLEISYRGIHSCSQAANVGT
TMPIQNLEPNQTQEHGNLDMVKESVDNYNHQAHLHHNLHYPLSSTPNLENNNAYMLQMRD
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FYS*

>G1931 (5..592)
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TCAGCTGGAGAACTTTCGAGGAGGTGGAGGAGAGATGGGAGGATTAGTGAGTAATAATAG
CAATAATAGTGATCATAATAAGAATTGCAACAAAGGAAAAGGGAAGAGAACTTTGGCAAT
GCAGAGGATAGCTTTTCATACAAGGAGTGATGATGATGTTCTTGATGATGGTTATCGTTG
GCGAAAGTACGGTCAGAAATCTGTCAAGAACAATGCTCATCCCAGGAGCTATTATAGATG
TACATACCACACATGCAACGTGAAGAAACAAGTGCAAAGACTGGCAAAAGATCCAAACGT
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>G1931 Amino Acid Sequence (domain in AA coordinates: 114-170)
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KYGQKSVKNNAHPRSYYRCTYHTCNVKKQVQRLAKDPNVVVTTYEGVHNHPCEKLMETLS
PLLRQLQFLSRVSDL*
>G2543 (1..2169)
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>G2543 Amino Acid Sequence (domain in AA coordinates: 31-91)
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KRSMMRLAQRMISNYCLSVSRSNNTRSTVVSELNEVGIRVTAHKSPEPNGTVLCAATTFW
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>G264 (30..1430)
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>G264 Amino Acid Sequence (domain in AA coordinates: 24-114)
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KKLLNFLETAIRNPTFVKNFGKKVEQLDISAYNKKRRLPEVEQSKPPSEDSHLDNSSGSS
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>G32 (101..736)
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>G32 Amino Acid Sequence (domain in aa coordinates: 17-84)
MNTTSSKSKKKQDDQVGTRFLGVRRRPWGRYAAEIRDPTTKERHWLGTFDTAEEAALAYD
RAARSMRGTRARTNFVYSDMPPSSSVTSIVSPDDPPPPPPPPAPPSNDPVDYMMMFNQYS
STDSPMLQPHCDQVDSYMFGGSQSSNSYCYSNDSSNELPPLPSDLSNSCYSQPQWTWTGD
DYSSEYVHSPMFSRMPPVSDSFPQGFNYFGS*
>G436 (1..2157)
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>G436 Amino Acid Sequence (domain in AA coordinates: 22-85)
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>G1909 Amino Acid Sequence (conserved domain in AA coordinates:23-51)
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>G1663 (64..630)
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>G1663 Amino Acid Sequence (domain in AA coordinates: TBD)
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>G1231 (103..870)
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>G1231 Amino Acid Sequence (domain in AA coordinates: TBD)
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>G227 (21..983)
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>G227 Amino Acid Sequence (domain in AA coordinates: 13-112)
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>G1842 (219..809)
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>G1842 Amino Acid Sequence (domain in AA coordinates: 2-57)
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ENGSGNKVPETLSLLK*
>G1505 (1..681)
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>G1505 Amino Acid Sequence (domain in AA coordinates: TBD)
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>G657 Amino Acid Sequence (domain in AA coordinates: TBD)
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>G1959 Amino Acid Sequence (conserved domain in AA coordinates:46-97)
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>G2180 (1..1440)
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>G2180 Amino Acid Sequence (conserved domain in AA coordinates:7-156)
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>G1817 (1..1308)
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>G1817 Amino Acid Sequence (conserved domain in AA coordinates:47-331)
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AYRKVIYFQSLISHL*
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>G1649 Amino Acid Sequence (conserved domain in AA coordinates:225-295)
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>G2131 Amino Acid Sequence (conserved domain in AA coordinates:50-186, 112-183)
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>G1508 Amino Acid Sequence (domain in AA coordinates: 38-63)
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>G2110 Amino Acid Sequence (conserved domain in AA coordinates:239-298)
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>G2442 (71..997)
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>G1052 Amino Acid Sequence (domain in AA coordinates 201-261)
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>G1079 Amino Acid Sequence (conserved domain in AA coordinates:1-50)

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>G1335 (56..667)

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ACGTTAAAACCAACGCCGGTTACGCGGTGGAGAAGAGTGAGTTGGTTATCTCACAAGTGA
TCGGTTCTTTCTCCCGCCGCCTTCTATCTCTCTATTATCCACTTTTTGCTTATTATGATG
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AAAAA

>G1335 Amino Acid Sequence (domain in AA coordinates: 24-43, 131-144, 185-203)

MSGDNGGGERRKGSVKWFDTQKGFGFITPDDGGDDLFVHQSSIRSEGFRSLAAEEAVEFE
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RGGGGRGGSDCYKCGEPGHMARDCSEGGGGYGGGGGGYGGGGGYGGGGGGYGGGGRGGGG
GGGSCYSCGESGHFARDCTSGGR*

>G157 (31..621)

GGGCATAACCCTTATCGGAGATTTGAAGCCATGGGAAGAAGAAAAATCGAGATCAAGCGA
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AAAGCTCGACAACTTTCGATTCTCTGTGAATCCTCCGTCGCTGTTGTCGTCGTATCTGCC
TCCGGAAAACTCTATGACTCTTCCTCCGGTGACGACATTTCCAAGATCATTGATCGTTAT
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AATGTAAGTGTAGATTCTCTAATTTCTCTGGAGGAACAACTTGAGACTGCTCTGTCCGTA
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AAATTGCTGAGAGAAGAGAACCAGGTTCTGGCTAGCCAGATGGGAAAGAATACGTTGCTG
GCAACAGATGATGAGAGAGGAATGTTTCCGGGAAGTAGCTCCGGCAACAAAATACCGGAG
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AGTGTTGTACCTCCTTCGGAGACAAGATCAGAGTTTGTGTGTTTGTGTCTGAATGTACGG
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>G157 Amino Acid Sequence (domain in AA coordinates: 2-57)
MGRRKIEIKRIENKSSRQVTFSKRRNGLIDKARQLSILCESSVAVVVVSASGKLYDSSSG
DDISKIIDRYEIQHADELRALDLEEKIQNYLPHKELLETVQSKLEEPNVDNVSVDSLISL
EEQLETALSVSRARKAELMMEYIESLKEKEKLLREENQVLASQMGKNTLLATDDERGMFP
GSSSGNKIPETLPLLN*
>G1895 (1..954)
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AGGACAAGAGACGAAACTTCTCATGAAACTGTTAAAGAGAGTAAAAATGCTTTTGAGAGA
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CATGTGTGGTATCCAGTACCGATGACCCGCGAGAAGACACAAGAATTCAGCTTTTTCAGT
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>G1895 Amino Acid Sequence (domain in AA coordinates: 55-110)
MNNQSVTDNTSLKLSSNLNNESKETSENSDDQHSEITTITSEEEKTTELKKPDKILPCPR
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TSEDTDNYNSSSTKILSFESSDSLVTERPKHQSNEVKINAEPVSQEPNNFQGLLPPQASP
VSPPWPYQYPPNPSFYHMPVYWGCAIPVWSTLDTSTCLGKRTRDETSHETVKESKNAFER
TSLLLESQSIKNETSMATNNHVWYPVPMTREKTQEFSFFSNGAETKSSNNRFVPETYLNL
QANPAAMARSMNFRESI*
>G1900 (1..897)
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AATAGGTTTGGTAATCAAAAGCTAGTTGCTAGGATAGAGAACAATGACGAGCGCTCTAAT
AACAACACTTCGAACGGTTTGAATTGTTTTCCGGGAGTTTCGTGGCCGTACACGTGGAAT
CCTGCGTTTTACCCGGTTTACCCTTATTGGAGCATGCCAGTGTTGTCTTCTCCGGTAAGT
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CTTTGTGCAAACCCTGCTGCGTTATCAAGATCAATCAATTTCCATGAGCAGATGTGA
>G1900 Amino Acid Sequence (domain in AA coordinates: 54-106)
MLETKDPAIKLFGMKIPFPTVLEVADEEEEKNQNKTLTDQSEKDKTLKKPTKILPCPRCN
SMETKFCYYNNYNVNQPRHFCKACQRYWTSGGTMRSVPIGAGRRKNKNNSPTSHYHHVTI
SETNGPVLSFSLGDDQKVSSNRFGNQKLVARIENNDERSNNNTSNGLNCFPGVSWPYTWN
PAFYPVYPYWSMPVLSSPVSSSPTSTLGKHSRDEDETVKQKQRNGSVLVPKTLRIDDPNE
AAKSSIWTTLGIKNEVMFNGFGSKKEVKLSNKEETETSLVLCANPAALSRSINFHEQM*
>G2007 (1..861)
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CTCCGACCTGACTTGAAGAGAGGTCTTCTCTCCGACGCCGAGGAACAGCTTGTCATCGAC
CTTCATGCTCTTCTCGGCAACAGATGGTCCAAGATCGCTGCAAGATTACCAGGAAGAACA
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AAGACGGGTCACAAGGACTAG
>G2007 Amino Acid Sequence (domain in AA coordinates: TBD)
MGRQPCCDKLMVKKGPWTAEEDKKLINFILTNGHCCWRALPKLAGLRRCGKSCRLRWTNY
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DYELLGDIIHNYGDLFNILWTNDEPPLVDDASWSNHNVGIGGTAAVAASDKNNTAAEEDF
PERSFEKQNGESWMFLDYCQEFGVEDFGFECYHGFGQSSMKTGHKD*
>G214 (238..2064)
TGAGATTTCTCCATTTCCGTAGCTTCTGGTCTCTTTTCTTTGTTTCATTGATCAAAAGCA
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GAATTAAAAATGGAATCTTTATCGAATCCAAGCTGATTTTGTTTCTTTCATTGAATCATC
TCTCTAAAGTGGAATTTTGTAAAGAGAAGATCTGAAGTTGTGTAGAGGAGCTTAGTGATG
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>G214 Amino Acid Sequence (domain in AA coordinates: 22-71)
METNSSGEDLVIKTRKPYTITKQRERWTEEEHNRFIEALRLYGRAWQKIEEHVATKTAVQ
IRSHAQKFFSKVEKEAEAKGVAMGQALDIAIPPPRPKRKPNNPYPRKTGSGTILMSKTGV
NDGKESLGSEKVSHPEMANEDRQQSKPEEKTLQEDNCSDCFTHQYLSAASSMNKSCIETS
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SSLSHPPSEPDSHPHTVAGDYQSFPNHIMSTLLQTPALYTAATFASSFWPPDSSGGSPVP
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LQHGSVQSREQEHSEASKARSSLDSEDVENKSKPVCHEQPSATPESDAKGSDGAGDRKQV
DRSSCGSNTPSSSDDVEADASERQEDGTNGEVKETNEDTNKPQTSESNARRSRISSNITD
PWKSVSDEGRIAFQALFSREVLPQSFTYREEHREEEQQQEQRYPMALDLNFTAQLTPVD
DQEEKRNTGFLGIGLDASKLMSRGRTGFKPYKRCSMEAKESRILNNNPIIHVEQKDPKRM
RLETQAST*
>G2155 (63..740)
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CATATTTGTAGTTTGATTTGACTATCCCCAAGTTTTGTATTTTATCATACAAATTTTTGC
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GAGATTGAATGTATAATATAATGGTTTAAT
>G2155 Amino Acid Sequence (domain in AA coordinates:18-38)
MLSKLPTQRHLHLSPSSPSMETVGRPRGRPRGSKNKPKAPIFVTIDPPMSPYILEVPSGN
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PLPPTSLSPPVSNFFTVSLAGPQGKVIGGFVAGPLVAAGTVYFVATSFKNPSYHRLPATE
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>G234 (106..1035)
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>G234 Amino Acid Sequence (domain in AA coordinates: 14-115)
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VYSDSKQFF*
>G361 (54..647)
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>G361 Amino Acid Sequence (domain in AA coordinates: 43-63)
MATETSSLKLFGINLLETTSVQNQSSEPRPGSGSGSESRKYECQYCCREFANSQALGGHQ
NAHKKERQLLKRAQMLATRGLPRHHNFHPHTNPLLSAFAPLPHLLSQPHPPPHMMLSPSS
SSSKWLYGEHMSSQNAVGYFHGGRGLYGGGMESMAGEVKTHGGSLPEMRRFAGDSDRSSG
IKLENGIGLDLHLSLGP*
>G562 (137..1285)
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TATAGTAGAGAGAGAGAGAGAGAGAGAGAGGTGTGATGATTATTGATCTATAAATTTTCGGA
GAGAGAGAGGGAGAAAGAGAAACTTTTCCTCCAGATGAAAATTTGGTGTTATGGTTTGTT
ACTGTTAATATAGAGAGGCTTTTCTTTTTTTATAAAATGGCTTCCTTTGTTGCA
>G562 Amino Acid Sequence (domain in AA coordinates: 253-315)
MGNSSEEPKPPTKSDKPSSPPVDQTNVHVYPDWAAMQAYYGPRVAMPPYYNSAMAASGHP
PPPYMWNPQHMMSPSGAPYAAVYPHGGGVYAHPGIPMGSLPQGQKDPPLTTPGTLLSIDT
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ADEPKLKRSREGTPTKDGKQLVQASSFHSVSPSSGDTGVKLIQGSGAILSPGVSANSNPF
MSQSLAMVPPETWLQNERELKRERRKQSNRESARRSRLRKQAETEELARKVEALTAENMA
LRSELNQLNEKSDKLRGANATLLDKLKCSEPEKRVPANMLSRVKNSGAGDKNKNQGDNDS
NSTSKFHQLLDTKPRAKAVAAG*
>G591 (88..1020)
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GCTCTAATGACTCTGGTTTCTTCTCTCCTCTCTCACCGACTTGAAAGGTAAAAAAGTGAA
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>G591 Amino Acid Sequence (domain in AA coordinates: 143-240)
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